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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 6, 2005, 05:47:32 ; Search time 181.5 Seconds  
(without alignments)  
6622.872 Million cell updates/sec

Title: US-10-032-254A-1

Perfect score: 2872

Sequence: 1 gttggagtcctcctcactc.....caaaaaaaaaaaaaaaaaa 1554

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DRV=xlp  
-Q=/cgn2\_1/USFTO.spool\_p/US10032254/runat\_02062005\_131018\_3585/app\_query.fasta\_1.1735  
-DB=A Geneseq\_16Dec04 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10032254 @CGN 1.1.154 @runat\_02062005\_131018\_3585 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A Geneseq\_16Dec04:\*  
1: Geneseqp19808:\*  
2: Geneseqp19908:\*  
3: Geneseqp20008:\*  
4: Geneseqp20018:\*  
5: Geneseqp20028:\*  
6: Geneseqp20038:\*  
7: Geneseqp20038s:\*  
8: Geneseqp20048s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match | Length | ID         | Description         |
|------------|--------|-------------|--------|------------|---------------------|
| 1          | 1808   | 63.0        | 358    | 2 AAW50159 | Aaw50159 Calmodulin |
| 2          | 1690   | 58.8        | 343    | 4 AAU03511 | Aau03511 Human pro  |
| 3          | 1673.5 | 58.3        | 372    | 5 ABP69106 | Abp69106 Human pol  |
| 4          | 1673.5 | 58.3        | 372    | 8 ADR39752 | Adr39752 Human kin  |
| 5          | 1625   | 56.6        | 343    | 2 AAW88436 | Aaw88436 Disease a  |
| 6          | 1625   | 56.6        | 343    | 8 ADL06509 | Adl06509 Human tum  |
| 7          | 1625   | 56.6        | 343    | 8 ADM72655 | Adm72655 Human TAS  |
| 8          | 1625   | 56.6        | 343    | 8 ADM72237 | Adm72237 Human TAS  |
| 9          | 1259   | 43.8        | 270    | 6 ABR41269 | Abr41269 Human DIT  |
| 10         | 1204   | 41.9        | 250    | 6 ABR41299 | Abr41299 Human DIT  |

|    |        |      |     |             |                     |
|----|--------|------|-----|-------------|---------------------|
| 11 | 1184.5 | 41.2 | 332 | 7 ADC15044  | Adc15044 Calcium/c  |
| 12 | 1184.5 | 41.2 | 370 | 6 AAE34492  | Aae34492 Human cam  |
| 13 | 1184.5 | 41.2 | 370 | 6 ADH23304  | Adh23304 Human cal  |
| 14 | 1184.5 | 41.2 | 370 | 8 ADL97820  | Adl97820 Human CAM  |
| 15 | 1184.5 | 41.2 | 370 | 8 ADP23704  | Adp23704 PRO polyp  |
| 16 | 1182.5 | 41.2 | 317 | 5 ABG69794  | Abg69794 Human CAM  |
| 17 | 1173.5 | 40.9 | 355 | 4 AAEL11777 | Aael11777 Human kin |
| 18 | 1173.5 | 40.9 | 355 | 4 AAU41268  | Aau41268 Human pol  |
| 19 | 1173.5 | 40.9 | 355 | 5 ABB08178  | Abb08178 Human cam  |
| 20 | 1173.5 | 40.9 | 357 | 4 AAE11768  | Aae11768 Human kin  |
| 21 | 1173.5 | 40.9 | 357 | 8 ADJ75440  | Adj75440 Marker ge  |
| 22 | 1173.5 | 40.9 | 357 | 8 ADQ15044  | Adq15044 Human can  |
| 23 | 1173.5 | 40.9 | 385 | 4 AAM39482  | Aam39482 Human pol  |
| 24 | 1173.5 | 40.9 | 385 | 4 AAB84359  | Aab84359 Amino aci  |
| 25 | 1169.5 | 40.7 | 355 | 4 AAB50055  | Aab50055 Murine De  |
| 26 | 1168.5 | 40.7 | 357 | 4 AAU03508  | Aau03508 Human pro  |
| 27 | 1157   | 40.3 | 356 | 4 AAB84360  | Aab84360 Amino aci  |
| 28 | 1112   | 38.7 | 355 | 8 ADI40885  | Adi40885 Human kin  |
| 29 | 1085.5 | 37.8 | 389 | 3 AAY68793  | Aay68793 Amino aci  |
| 30 | 1070   | 37.3 | 503 | 4 ABG05970  | Abg05970 Novel hum  |
| 31 | 1065   | 37.1 | 460 | 5 ABG69792  | Abg69792 Human CAD  |
| 32 | 1065   | 37.1 | 476 | 5 AAE22764  | Aae22764 Human cal  |
| 33 | 1065   | 37.1 | 476 | 5 ABG69793  | Abg69793 Human CAD  |
| 34 | 1065   | 37.1 | 476 | 7 ADE56391  | Ade56391 Human Pro  |
| 35 | 1065   | 37.1 | 476 | 7 ADE56387  | Ade56387 Human Pro  |
| 36 | 1065   | 37.1 | 476 | 7 ADD45328  | Add45328 Human pro  |
| 37 | 1065   | 37.1 | 497 | 4 AAM41547  | Aam41547 Human pol  |
| 38 | 1051.5 | 36.6 | 567 | 4 AAM39761  | Aam39761 Human pol  |
| 39 | 1028.5 | 35.8 | 309 | 7 ADSE6389  | Adse6389 Rat Prote  |
| 40 | 1028.5 | 35.8 | 309 | 7 ADD45326  | Add45326 Rat Prote  |
| 41 | 1028.5 | 35.8 | 309 | 7 ADE56385  | Ade56385 Rat Prote  |
| 42 | 1028.5 | 35.8 | 309 | 7 ADD46031  | Add46031 Rat Prote  |
| 43 | 1017.5 | 35.4 | 326 | 6 AAE32426  | Aae32426 Human kin  |
| 44 | 1017.5 | 35.4 | 326 | 8 ADE28335  | Ade28335 Human KPP  |
| 45 | 1017.5 | 35.4 | 326 | 8 ADH23302  | Adh23302 Novel hum  |

#### ALIGNMENTS

RESULT 1

AAW50159  
ID AAW50159 standard; protein; 358 AA.

XX AC AAW50159;

XX DT 09-JUL-1998 (first entry)

XX DE Calmodulin-dependent protein kinase clone 29.

XX KW Rat; calmodulin-dependent protein kinase; clone 29.

XX OS Rattus rattus.

XX FH Key Location/Qualifiers

FT Misc-difference 344

FT /note= "encoded by TG"

XX PN W09805352-A1.

XX PD 12-FEB-1998.

XX PF 01-AUG-1997; 97WO-US013657.

XX PR 02-AUG-1996; 96US-0023220P.

XX PA (SCRI ) SCRIPPS RES INST.

XX PI Sutcliffe JG, Gautvik KM, De Lecea L, Bloom PE, Danielson PE;

XX PI Gautvik VT, Kilduff TS, Foye PE;

XX DR WPI; 1998-145352/13.

XX DR N-PSDB; AAV18867.

XX XX

PT Nucleic acid encoding hypocretin of rat and mouse - useful for diagnosis  
PT and treatment of neurological disease, homeostatic dysfunction etc., also  
PT sequence for calmodulin kinase-like protein.

XX Disclosure; Fig 6; 11pp; English.

CC The present sequence is rat calmodulin-dependent protein kinase clone 29.

XX SQ Sequence 358 AA;

Alignment Scores:  
Pred. No.: 2,26e-141 Length: 358  
Score: 1808.00 Matches: 353  
Percent Similarity: 98.60% Conservative: 0  
Best Local Similarity: 98.60% Mismatches: 5  
Query Match: 62.95% Indels: 1  
DB: 2 Gaps: 0

US-10-032-254A-1 (1-1554) x AAWS0159 (1-358)

QY 105 ATGCTGCTCTCAAGAAACAGACGAGGACATCAGCAGTGTCTATCAGATCCGGGAGAAG 164  
Db |||||||  
1 MetLeuLeuLeuLysGlnThrGluAspIleSerSerValTyrGluIleArgGluLys 20  
QY 165 CTGGGCTCGGGTCCTCTCTGAGGTGATGCTGGCCAGGAAAGGGCTCTGCTCATCTT 224  
Db |||||||  
21 LeuGlySerGlyAlaPheSerGluValMetLeuAlaGlnGluArgGlySerAlaHisLeu 40  
QY 225 GTGGCCCTCAAGTGCAATCCCAAGAACGACTTCGGGGCAAGGAGCCCTGGTGGAGAAT 284  
Db |||||||  
41 ValAlaLeuLysCysIleProLysLysAlaLeuArgGlyLysGluAlaLeuValGluAsn 60  
QY 285 GAGATCGCGTACTTCGCGAATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTCAT 344  
Db |||||||  
61 GluIleAlaValLeuArgGlnSerHisProAsnIleValAlaLeuGluAspValHis 80  
QY 345 GAGAGTCTTCTCATCTACTTGGCCATGGAGCTGTAAACAGTGGTGAACCTTTTGAC 404  
Db |||||||  
81 GluSerProSerHisLeuTyrLeuAlaMetGluLeuValThrGlyGlyGluLeuPheAsp 100  
QY 405 CGCATCATGAGCGGGCTCTACACAGAGAAGCGCCAGCCACCTTGTAGGGCAGGTC 464  
Db |||||||  
101 ArgIleMetGluArgGlySerTyrThrGluLysAspAlaSerHisLeuValGlyGlnVal 120  
QY 465 CTTGGCGCTCTCTACCTTCTATAGCTGGGATCGTCACCGGACCTCAAGCCCTGAA 524  
Db |||||||  
121 LeuGlyAlaValSerTyrLeuHisSerLeuGlyIleValHisArgAspLeuLysProGlu 140  
QY 525 AACCTCTCTATGCCACACCTTTTGGAGCTCCAAGATCATGTCTCTGACCTTTGGCCTG 584  
Db |||||||  
141 AsnLeuLeuTyrAlaThrProPheGluAspSerLysIleMetValSerAspPheGlyLeu 160  
QY 585 TCCAAATACAAAGTGGCAATCTAGGACAGCCTGTGGGACCCAGGATATGTGGCC 644  
Db |||||||  
161 SerLysIleGlnAlaGlyAsnMetLeuGlyThrAlaCysGlyThrProGlyTyrValAla 180  
QY 645 CCAGAGTCTCTGGAGCAGAAACCTTACGGGAAGCCGTAGATGTGGGCCCTGGGTGTC 704  
Db |||||||  
181 ProGluLeuLeuGluGlnLysProTyrGlyLysAlaValAspValTrpAlaLeuGlyVal 200  
QY 705 ATCTCTACATCTGTGTGGGTACCCCTTCTATCATCAGACGATCTCTGAACTC 764  
Db |||||||  
201 IleSerTyrIleLeuLeuLysGlyTyrProPheTyrAspGluSerAspProGluLeu 220  
QY 765 TTGAGCCAGATCTTGAGGGCCAGCTAGCTTTGACTCCCTCTTTGGGATGACATCTCA 824  
Db |||||||  
221 PheSerGlnIleLeuArgAlaSerTyrGluPheAspSerProPheTrpAspIleSer 240  
QY 825 GAATACGCCAAAGACTTTCATTCGCCACCTTCTGGAACGTGATCCCCAGAGAGGTTCCAC 884  
Db |||||||  
241 GluSerAlaLysAspPheIleArgHisLeuLeuGluArgAspProGlnLysArgPheThr 260  
QY 885 TGCAGCAGGCCCTTACAGCATCTTTGGATCTCTGGGGATGCAGCCCTTCGATAGGGACATC 944

Db |||||||  
261 CysGlnGlnAlaLeuGlnHisLeuTrpIleSerGlyAspAlaAlaLeuAspArgPheIle 280  
QY 945 CTGGGTTCCTGTCAGTCAGCAGATCCAGAAGATTTTGCAGGACCCACTGGAGCGTGCA 1004  
Db |||||||  
281 LeuGlySerValSerGluGlnIleGlnLysAsnPheAlaArgThrHisTrpLysArgAla 300  
QY 1005 TTCATATGCCACATCATCTCTACGTACATCCCTAAGCTGGGACAAAGCCAGAGGGTGAG 1064  
Db |||||||  
301 PheAsnAlaThrSerPheLeuArgHisIleArgLysLeuGlyGlnSerProGluGlyGlu 320  
QY 1065 GAGGCTCCAGCAGCTGTATGACCCGTATACCCACCCAGGCGCTGGGACTAGCCAGTCC 1124  
Db |||||||  
321 GluAlaSerArgGlnGlyMetThrArgHisSerHisProGlyLeuGlyThrSerGlnSer 340  
QY 1125 CCCAAGTGGTG-AAAACACGAGTAGATGCCAAGGAAGCCCAAGTGGAGTCACTCC 1177  
Db |||||||  
341 ProLysTrpValThrThrArgTrpMetProArgLysAlaLysTrpThrAspSer 358  
RESULT 2  
AAU03511  
ID AAU03511 standard; protein; 343 AA.  
XX  
AC AAU03511;  
XX 12-SEP-2001 (first entry)  
DE Human protein kinase #11.  
XX Human; protein kinase; PTK; STK; cancer; cardiovascular disease;  
KW metabolic disorder; immune related disease; neurological disorder;  
KW neurodegenerative disorder; inflammatory disorder; infectious disease;  
KW reproductive disorder.  
XX  
OS Homo sapiens.  
XX WO200138503-A2.  
XX  
PD 31-MAY-2001.  
XX  
PF 22-NOV-2000; 2000WO-US032085.  
XX  
PR 24-NOV-1999; 99US-0167482P.  
XX (SUGS-) SUGEN INC.  
PA Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;  
PI Flanagan P, Clary D;  
PI  
XX WPI; 2001-343950/36.  
DR N-P8DB; AAS06711.  
XX  
PT Nucleic acids encoding human kinase polypeptides, useful for preventing  
diagnosing and/or treating e.g. cancer, immune, cardiovascular and  
PT neuronal-associated diseases, and microbial infections.  
PT  
XX Claim 7; Fig 2; 43pp; English.  
PS  
XX AAU03501-AAU03557 represent novel human protein kinases #1-57. The novel  
protein kinases have been identified as members of the tyrosine or  
CC serine/threonine kinase (PTK and STK) families. The polynucleotides  
encoding protein kinases and the polypeptides may be used in the  
CC prevention, diagnosis and treatment of diseases associated with  
CC inappropriate kinase expression. For example, they may be used to treat  
CC cancers (especially cancers of haematopoietic origin), cardiovascular  
CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),  
CC immune related diseases (e.g. rheumatoid arthritis), neurological  
CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.  
CC Parkinson's disease), inflammatory disorders (e.g. asthma), infectious  
CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).  
CC Additionally, polynucleotides encoding protein kinases may be used for  
CC gene therapy and as DNA probes in diagnostic assays. The protein kinase  
CC polypeptides may be used as antigens in the production of antibodies

|          |      |   |      |
|----------|------|---|------|
| Db       | 281  | LeuGlySerValSerGluGlnIleArgLysAsnPheAlaArgThrHisTrpLysArgAla              | 300  |
| Qy       | 1005 | TTCAATGCCACATCATTTCTTACCTGCATCCGTAAGCTGGGACAAAGCCACAGAGGTGAG              | 1064 |
| Db       | 301  | PheAsnAlaThrSerPheLeuArgHisIleArgLysLeuGlyGlnIleProGluGlyGlu              | 320  |
| Qy       | 1065 | GAGCGCTCCAGGCAGTGTATGACCCGTCATAGCCACCCAGGCCCTTGGGACTAGCCAGTCC             | 1124 |
| Db       | 321  | GlyAlaSerGluGlnGlyMetAlaArgHisSerHisSerGlyLeuArgAlaGlyGlnPro              | 340  |
| Qy       | 1125 | CCCAAGTGG   | 1133 |
| Db       | 341  | ProlysTrp   | 343  |
| RESULT 3 |      |   |      |
| ABP69106 | ID   | ABP69106 standard; protein; 372 AA.                                       |      |
| XX       | AC   | ABP69106;   |      |
| XX       | XX   | 20-JAN-2003 (first entry)   |      |
| DT       | XX   | Human polypeptide SEQ ID NO 1153.   |      |
| DE       | XX   | Human; genome mapping; gene therapy; food supplement; virus; fungus;      |      |
| XX       | KW   | cell-proliferative disorder; neurodegenerative disease; bacterial;        |      |
| KW       | KW   | Parkinson's disease; Alzheimer's disease; autoimmune disease;             |      |
| KW       | KW   | multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;   |      |
| KW       | KW   | arthritis; cytostatic; immunomodulator; neotropic; neuroprotective;       |      |
| KW       | KW   | antiparkinsonian; antidiabetic; immunosuppressive; dermatological;        |      |
| KW       | KW   | haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;   |      |
| KW       | XX   | antiarthritic.  |      |
| XX       | OS   | Homo sapiens.   |      |
| XX       | XX   | WO200270539-A2.   |      |
| XX       | PD   | 12-SEP-2002.  |      |
| XX       | XX   | 05-MAR-2002; 2002WO-US0005095.  |      |
| PF       | PF   | 05-MAR-2001; 2001US-00799451.   |      |
| XX       | XX   | (HYSE-) HYSEQ INC.  |      |
| XX       | PA   | Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;          |      |
| PI       | PI   | Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;                |      |
| PI       | PI   | Wehrman T, Wang J, Wang D, Drmanac RT;                                    |      |
| XX       | XX   | WPI; 2002-759812/82.  |      |
| DR       | DR   | N-PSDB; ABZ11323.   |      |
| XX       | XX   | New polynucleotides comprising sequences assembled from expressed         |      |
| PT       | PT   | sequence tags (ESTs), useful for treating cell-proliferative,             |      |
| PT       | PT   | neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet  |      |
| PT       | PT   | or coagulation disorders.   |      |
| XX       | XX   | Claim 9; SEQ ID NO 1153; 1012pp + Sequence Listing; English.              |      |
| PS       | PS   | The invention relates to an isolated polynucleotide (I) comprising a      |      |
| XX       | XX   | nucleotide sequence selected from any of 948 sequences (ABZ11119-         |      |
| CC       | CC   | ABZ112066) or their mature protein coding portion, active domain coding   |      |
| CC       | CC   | protein or complementary sequences. The polynucleotides are useful for    |      |
| CC       | CC   | identifying expressed genes or for physical mapping of human genome. The  |      |
| CC       | CC   | encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight   |      |
| CC       | CC   | markers, as a food supplement, for generating antibodies, in medical      |      |
| CC       | CC   | imaging, screening and diagnostic assays and for treating cell-           |      |
| CC       | CC   | proliferative disorders (cancer), neurodegenerative diseases (Parkinson's |      |
| CC       | CC   | or Alzheimer's disease), autoimmune diseases (multiple sclerosis,         |      |
| CC       | CC   | diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,        |      |
| CC       | CC   | platelet or coagulation disorders, wound, burns, incision, ulcers, liver  |      |
| CC       | CC   | or lung fibrosis, infections (bacterial, viral, fungal, parasitic),       |      |
| CC       | CC   | arthritis, etc. Note: The sequence data for this patent did not form part |      |

CC of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 372 AA;

Alignment Scores:

Pred. No.: 3 54e-130 Length: 372  
Score: 1673.50 Matches: 327  
Percent Similarity: 88.98% Conservative: 4  
Best Local Similarity: 87.90% Mismatches: 12  
Query Match: 58.27% Indels: 29  
DB: 5 Gaps: 1

US-10-032-254A-1 (1-1554) x ABP69106 (1-372)

```
QY 105 ATGCTGCTCTCAAGAAACAGCGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAG 164
DB 1 MetLeuLeuLeuLysHisThrGluAspIleSerSerValTyrGluIleArgGluArg 20
QY 165 CTGGGCTCG----- 173
DB 21 LeuGlySerGlyProSerProLeuHisSerLeuSerLeuProLeuLeuSerSerHis 40
QY 174 -----GGTGCCTTCTCTGAGGTGATGCTG 197
DB 41 PheLeuProThrSerHisArgProValCysGlyArgGlyAlaPheSerGluValValLeu 60
QY 198 GCCAGAAAGGGCTCTCTCATCTTGTGGCCCTCAAGTGCATTCCTCAAGAAAGCACTT 257
DB 61 AlaGlnGluArgGlySerAlaHisLeuValAlaLeuLysCysIleProLysLysAlaLeu 80
QY 258 CGGGCAAGAGGCCCTGTGGAGATGAGATCGCGTACTTCGAGATCAGCCATCCC 317
DB 81 ArgGlyLeuGluAlaLeuValGluAenGluIleAlaValLeuArgArgIleSerHisPro 100
QY 318 AACATTGTGGCTCTCGAGAGCGTCCATGAGAGTCTCTCATCTCTACTTGGCCATGGAG 377
DB 101 AsnIleValAlaLeuGluAspValHisGluSerProSerHisLeuTyrLeuAlaMetGlu 120
QY 378 CTGGTAACAGGTGGTGAACCTTTGACCGCATCATGAGCGGGCTCTTACACAGAGAAG 437
DB 121 LeuValThrGlyGlyGluLeuPheAspArgIleMetGluArgGlySerTyrThrGluLys 140
QY 438 GACCCAGCACCTTGTAGCGCAGGTCTTGGCGTGTCTCTACCTTCATAGCCTGGGC 497
DB 141 AspAlaSerHisLeuValGlyGlnValLeuGlyAlaValSerTyrLeuHisSerLeuGly 160
QY 498 ATCGTCCACCGGACCTCAAGCCTGAAACCTCTCTATGCCACACCTTTTGAGGACTCC 557
DB 161 IleValHisArgAspLeuLysProGluAenLeuLeuTyrAlaThrProPheGluAspSer 180
QY 558 AAGATCATGTCTCTGACCTTTGGCTGTGCCAATACAAAGCTGSCAACATGCTAGGCACA 617
DB 181 LysIleMetValSerAspPheGlyLeuSerLysIleGlnAlaGlyAsnMetLeuGlyThr 200
QY 618 GCCTGTGGACCCACAGATATGCGCCACAGACTCTCTGAGCAGAGAACCTTACGGGAAG 677
DB 201 AlaCysGlyThrProGlyTyrValAlaProGluLeuGluGlnLysProTyrGlyLys 220
QY 678 GCGGTAGATGTGTGGGCCCTGGGTGTCTCTCATCTCTATCTGTGTGGTACCCCCC 737
DB 221 AlaValAspValTrpAlaLeuGlyValIleSerTyrIleLeuLeuGlyTyrProPro 240
QY 738 TTCTATGATGAGCGCATCCTGAACCTTTTCAGCAGATTTCTGAGGCCAGCTATGAGTTT 797
DB 241 PheTyrAspGluSerAspProGluLeuPheSerGlnIleLeuArgAlaSerTyrGluPhe 260
QY 798 GACTCCCCCTTTGGGATGACATCTCAGATAGCCAAAGACTTCATTGCGCACTTCG 857
DB 261 AspSerProPheTrpAspIleSerGluSerAlaLysAspPheIleArgHisLeuLeu 280
QY 858 GAACGTGATCCCCAGAAAGGTTTCACCTGCCAGCAGCCCTCAGCATCTTTGGATCTCT 917
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DB 281 GluArgAspProGlnLysArgPheThrCysGlnGlnAlaLeuArgHisLeuTrpIleSer 300
QY 918 GGGATGACAGCCTTCGATAGGACATCTCTGGGTTCTGTCTGTCAGTCCAGAGAAAT 977
DB 301 GlyAspThrAlaPheAspArgAspIleLeuGlySerValSerGluGlnIleArgLysAsn 320
QY 978 TTTTGCAGGACCCACTGGAAGCGTGCATTCAATCCACATCATTCCTAGCTCACATCCGT 1037
DB 321 PheAlaIaArgThrHisTrpLysArgAlaPheAsnAlaThrSerPheLeuArgHisIleArg 340
QY 1038 AAGCTGGGACAAAGCCAGAGGGTGTAGGAGGCTCCAGGCAGTGTATGACCCCTCATAGC 1097
DB 341 LysLeuGlyGlnIleProGluGlyAlaSerGluGlnGlyMetAlaArgHisSer 360
QY 1098 CACCCAGGCTTGGGACTAGCCAGTCCCTCCCAAGTGG 1133
DB 361 HisSerGlyLeuArgAlaGlyGlnProProLysTrp 372
RESULT 4
ADR39752
ID ADR39752 standard; protein; 372 AA.
AC ADR39752;
DT XX
DT 18-NOV-2004 (first entry)
XX DE Human kinase and phosphatase KPP-25 protein SEQ ID NO:25.
XX human; kinase and phosphatase protein; KPP; enzyme; cytostatic;
KW antiarteriosclerotic; anticonvulsant; neurotropic; neuroprotective;
KW cerebroprotective; anti-HIV; antiallergic; antiinflammatory;
KW thymomimetic; gene therapy; cell proliferative disorder; cancer;
KW atherosclerosis; neurological disorder; epilepsy; Huntington's disease;
KW stroke; immune disorder; inflammatory disorder; AIDS; allergy;
KW developmental disorder; Hypothyroidism; Cushing's syndrome; infection;
KW KPP-25.
XX Homo sapiens.
XX WO2004074453-A2.
XX 02-SEP-2004.
XX 20-FEB-2004; 2004WO-US005092.
XX 20-FEB-2003; 2003US-0449059P.
PR 19-MAR-2003; 2003US-0456932P.
PR 28-MAR-2003; 2003US-0458844P.
PR 09-APR-2003; 2003US-0461678P.
PR 17-APR-2003; 2003US-0463937P.
XX (INCY-) INCYTE CORP.
PA RamKumar J, Marquis JP, Swarnakar A, Chawla NK, Tran UK;
XX Becha SD, Lee SY, Hafalia AJA, Richardson TW, Khare R, Jiang X;
PI Jackson AA, Yang J, Gorvad AE;
XX WPI; 2004-635568/61.
DR N-PSDB; ADR39798.
XX New human kinases and phosphatases (KPP) for diagnosing, treating and
PT preventing diseases or conditions associated with aberrant KPP expression
PT e.g. cancer, acquired immunodeficiency syndrome, epilepsy, or infections.
XX Claim 1; SEQ ID NO 25; 299pp; English.
XX The present sequence represents the human kinase and phosphatase protein
CC (KPP), designated KPP-25. The human KPP sequences from the present
CC invention have cytostatic, antiarteriosclerotic, anticonvulsant,
CC neurotropic, neuroprotective, cerebroprotective, anti-HIV, antiallergic,
CC antiinflammatory and thymomimetic activities, and can be used in gene
CC therapy. The human KPP proteins and polynucleotides can be used in
CC diagnosing, treating and preventing diseases or conditions associated
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CC with the decreased expression or overexpression of KPP, such as cell  
CC proliferative (e.g. cancer, atherosclerosis), neurological (e.g.  
CC epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS,  
CC allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome)  
CC disorders, or infections. They can also be used in assessing the effects  
CC of exogenous compounds on the expression of nucleic acid and amino acid  
CC sequences of KPP. The KPP or its fragments are useful in screening  
CC compounds for effectiveness as agonist or antagonist of the polypeptides,  
CC or in altering the expression of the target polynucleotide and compounds  
CC that specifically bind to or modulate the activity of the polypeptide.

XX  
SQ Sequence 372 AA;

#### Alignment Scores:

Pred. No.: 3,54e-130 Length: 372  
Score: 1673.50 Matches: 327  
Percent Similarity: 88.98% Conservative: 4  
Best Local Similarity: 87.90% Mismatches: 12  
Query Match: 58.27% Indels: 29  
DB: Gaps: 1

US-10-032-254A-1 (1-1554) x ADR39752 (1-372)

```
QY 105 ATGCTCTCTCTCAGAAACAGACGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAG 164
    |||
DB 1 MetLeuLeuLeuLysLysHisThrGluAspIleSerSerValTyrGluIleArgGluArg 20
    |||
QY 165 CTGGGCTCG----- 173
    |||
DB 21 LeuGlySerGlyProSerProLeuHisSerLeuSerLeuLeuProLeuLeuSerSerHis 40
    |||
QY 174 -----GGTGCCTTCTCTCAGGTGATGCTG 197
    |||
DB 41 PheLeuProThrSerHisArgProValCysGlyArgGlyAlaPheSerGluValValLeu 60
    |||
QY 198 GCCAGGAAGGGCTCTGCTCATCTTGTGGCCCTCAAGTGCATTCCTCCAGAAAGCACTT 257
    |||
DB 61 AlaGlnGluArgGlySerAlaHisLeuValAlaLeuLysCysIleProLysLysAlaLeu 80
    |||
QY 258 CGGGCAAGGAGCCCTGTGGAGATGAGATCGCGTACTTCGCGAGAATCAGCCATCCC 317
    |||
DB 81 ArgGlyLysGluAlaLeuValGluAenGluIleAlaValLeuArgIleSerHisPro 100
    |||
QY 318 AACATTGTGGCTCTGGAGACGCTCCATGAGAGTCTTCTCATCTCTACTTGGCCATGGAG 377
    |||
DB 101 AenIleValAlaLeuGluAspValHisGluSerProSerHisLeuTyrLeuAlaMetGlu 120
    |||
QY 378 CTGGTAACAGGTGGTGAATCTTTTACCGCATCATGAGCGGGCTCTTACACAGAGAAG 437
    |||
DB 121 LeuValThrGlyGlyGluLeuPheAspArgIleMetGluArgGlySerTyrThrGluLys 140
    |||
QY 438 GACCCAGCCACCTTGTAGGGCAGGTCTTGGCGCTGTCTCTACCTCATAGCTGGGC 497
    |||
DB 141 AspAlaSerHisLeuValGlyGlnValLeuGlyAlaValSerTyrLeuHisSerLeuGly 160
    |||
QY 498 ATCGTGACCGGACCTCAAGCCTGAAACCTCTCTATGCCACACCTTTTGGAGCTCC 557
    |||
DB 161 IleValHisArgAspLeuLysProGluAenLeuTyrAlaThrProPheGluAspSer 180
    |||
QY 558 AAGATCATGGTCTCTGACTTTGGCCTGTCCAAATACAAAGCTGGCAACATGCTAGGCACA 617
    |||
DB 181 LysIleMetValSerAspPheGlyLeuSerLysIleGlnAlaGlyAenMetLeuGlyThr 200
    |||
QY 618 GCTGTGGGACCCAGATATGTGGCCGACAGCTCTGGAGCAGAAACCCCTACGGGAG 677
    |||
DB 201 AlaCysGlyThrProGlyTyrValAlaProGluLeuLeuGlnLysProTyrGlyLys 220
    |||
QY 678 GCCGTAGATGTGTGGCCCTGGGTGTCTCTCTACATCTGTGTGTGGTACCCCCC 737
    |||
DB 221 AlaValAspValIleAlaLeuGlyValIleSerTyrIleLeuLeuCysGlyTyrProPro 240
    |||
QY 738 TTCTATGATGAGCGCATCTGAACTCTTTCAGGCAGATTTCTGAGGGCCAGCTATGATTT 797
    |||
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```
DB 241 PheTyrAspGluSerAspProGluLeuPheSerGlnIleLeuArgAlaSerTyrGluPhe 260
QY 798 GACTCCCCCTTTTGGGATGACATCTCAGAAATCAGCCAAAGACTTTCATTCGCCACCTTCTG 857
    |||
DB 261 AspSerProPheTyrAspAspIleSerGluSerAlaLysAspPheIleArgHisLeuLeu 280
    |||
QY 858 GAACGTGATCCCGAGAGAGGTTCACCTGCCAGCAGGCCCTACAGCATCTTTGGATCTCT 917
    |||
DB 281 GluArgAspProGlnLysArgPheThrCysGlnGlnAlaLeuArgHisLeuTyrIleSer 300
    |||
QY 918 GGGGATGACGCTTCGATAGGACATCCTGGGTCTGTGTCAGTGAGCAGATCCAGAGAAT 977
    |||
DB 301 GlyAspThrAlaPheAspArgAspIleLeuGlySerValSerGluGlnIleArgLysAen 320
    |||
QY 978 TTTGCCAGGACCCACTGGAAGCGTGCATTCATCAATGCCACATCATTCCTACGTCATCCGT 1037
    |||
DB 321 PheAlaArgThrHisTyrLysArgAlaPheAenAlaThrSerPheLeuArgHisIleArg 340
    |||
QY 1038 AAGCTGGGACAAAGCCAGAGGTGAGGAGGCTCCAGGAGTGTATGACCCGTCATAGC 1097
    |||
DB 341 LysLeuGlyGlnIleProGluGlyGluGlyAlaSerGluGlnGlyMetAlaArgHisSer 360
    |||
QY 1098 CACCCAGGCTTGGGACTAGCCAGTCCCAAGTGG 1133
    |||
DB 361 HisSerGlyLeuArgAlaGlyGlnProProLysTyr 372
    |||
RESULT 5
AAW88436
ID AAW88436 standard; protein; 343 AA.
XX
AC AAW88436;
XX
DT 26-APR-1999 (first entry)
XX
DE Disease associated protein kinase DAPK-5.
XX
KW DAPK-5; disease associated protein kinase; human; diagnosis; therapy;
KW adult respiratory distress syndrome; allergy; asthma; arteriosclerosis;
KW bronchitis; emphysema; hyper eosinophilia; myocardial inflammation;
KW pericardial inflammation; anaemia; rheumatoid arthritis;
KW Addison's disease; AIDS; atherosclerosis; atopic dermatitis;
KW dermatomyositis; diabetes mellitus; glomerulonephritis; gout;
KW Grave's disease; lupus erythematosus; multiple sclerosis;
KW myasthenia gravis; osteoarthritis; osteoporosis; pancreatitis;
KW polycystic kidney disease; polymyositis; scleroderma;
KW Sjogren's syndrome; autoimmune thyroiditis; cancer; infection; trauma;
KW cell proliferation.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Binding-site 22..294 /note= "potential ATP binding site"
FT Peptide 134..141 /note= "catalytic loop"
FT Modified-site 171 /note= "putative phosphorylation site"
FT Misc-difference 233 /note= "encoded by TNT"
FT Misc-difference 328 /note= "encoded by GSC"
FT Misc-difference 329 /note= "encoded by CGN"
FT Misc-difference 333 /note= "encoded by TNA"
XX
PN WO9858052-A2.
XX
PD 23-DEC-1998.
XX
PF 19-JUN-1998; 98WO-US012813.
XX
PR 19-JUN-1997; 97US-00878989.
```

XX (INCY-) INCYTE PHARM INC.  
XX Bandman O, Hillman JL, Corley NC, Guegler KJ, Lal P, Goli SK;  
PI Shah P;  
XX WPI: 1999-080952/07.  
DR N-PSDB; AAX06835.  
XX New disease associated protein kinases - used to stimulate cell  
PT proliferation and to treat the immune response and cancer.  
XX Claim 1; Page 59-60; 93pp; English.  
XX This is the amino acid sequence of human disease associated protein  
CC kinase DAPK-5, as deduced from a consensus sequence (see AAX06835) of  
CC overlapping cDNA clones from libraries which are immortalised or  
CC cancerous. DAPK-5 shows 64% homology to human Cam-kinase, CamKI (GI  
CC 790790). The invention provides DAPK-1 to DAPK-7 polypeptides (see  
CC AAX88432-38) and cDNA clones encoding them (see AAX06831-36 and  
CC AAX06882), as well as expression vectors, host cells, agonists,  
CC antagonists and antibodies. The invention further provides uses of such  
CC products in the diagnosis, prevention and treatment of diseases  
CC associated with cell proliferation, especially cancer or an immune  
CC response (claimed). Conditions that may be treated include adult  
CC respiratory distress syndrome, allergies, asthma, arteriosclerosis,  
CC bronchitis, emphysema, hyper eosinophilia, myocardial or pericardial  
CC inflammation, rheumatoid arthritis, Addison's disease, AIDS, anaemia,  
CC atherosclerosis, various diseases of the digestive system, atopic  
CC dermatitis, dermatomyositis, diabetes mellitus, glomerulonephritis, gout,  
CC Grave's disease, lupus erythematosus, multiple sclerosis, myasthenia  
CC gravis, osteoarthritis, osteoporosis, pancreatitis, polycystic kidney  
CC disease, polymyositis, scleroderma, Sjogren's syndrome, autoimmune  
CC thyroiditis, complications of cancer, extracorporeal circulation, viral,  
CC bacterial, fungal, parasitic, protozoal and helminthic infections, and  
CC trauma (disclosed)  
XX Sequence 343 AA;

Alignment Scores:  
Pred. No.: 3,73e-126 Length: 343  
Score: 1695.00 Matches: 316  
Percent Similarity: 93.29% Conservative: 4  
Best Local Similarity: 92.13% Mismatches: 23  
Query Match: 56.58% Indels: 0  
DB: 2 Gaps: 0

US-10-032-254A-1 (1-1554) x AAX88436 (1-343)

QY 105 ATCTGCTGCTCAAGAAACAGACGGAGGACATCAGAGTGTCTATGAGATCCGGAGAG 164  
Db 1 MetLeuLeuLeuLysHisThrGluAspIleSerSerValTyrGluIleArgGluArg 20  
QY 165 CTGGGCTCGGGTCCCTTCTCTGAGGTGATGCTGGCCAGGAAAGGGCTCTGCTCATCTT 224  
Db 21 LeuGlySerGlyAlaPheSerGluValValLeuAlaGlnGluArgGlySerAlaHisLeu 40  
QY 225 GTGGCCCTCAAGTGCATTTCCAAAGAACGACTTTCGGGGCAAGGAGCCCTGTGGAGAAT 284  
Db 41 ValAlaLeuLysCysIleProLysLysAlaLeuArgGlyLysGluAlaLeuValGluAsn 60  
QY 285 GAGATCGGGTACTTCGCAGAAATCCAGCATCCCAACATTGTGGCTCTGGAGGACGTCCAT 344  
Db 61 GluIleAlaValLeuArgArgIleSerHisProAsnIleValAlaLeuGluAspValHis 80  
QY 345 GAGAGTCTTCTCATCTCTACTTTGGCCATCGAGCTGGTAACAGTGTGTGAACCTTTTGC 404  
Db 81 GluSerProSerHisLeuTyrLeuAlaMetGluLeuValThrGlyGlyGluLeuPheAsp 100  
QY 405 CGCATCATGGAGCGGGCTCTCTACACAGAGAAGAGCCAGCCACTTGTAGCGCAGGTC 464  
Db 101 ArgIleMetGluArgGlySerTyrThrGluLysAspAlaSerHisLeuValGlyGlnVal 120

QY 465 CTGGCGCTGTCTCTTACCTTCATAGCTGGGCATCGTCACGGACCTCAAGCCTGAA 524  
Db 121 LeuGlyAlaValSerTyrLeuHisSerLeuGlyIleValHisArgAspLeuLysProGlu 140  
QY 525 AACCTCTCTATGCCCACACCTTTTGAGGACTCCAAGATCATGCTCTCTCACTTTGGCCTG 584  
Db 141 AsnLeuLeuTyrAlaThrProPheGluAspSerLysIleMetValSerAspPheGlyLeu 160  
QY 585 TCAAAATATCAAGCTGGGCAACATGTAGGCACAGCCTGTGGGACCCAGCATATGTGGCC 644  
Db 161 SerLysIleGlnAlaGlyAsnMetLeuGlyThrAlaCysGlyThrProGlyTyrValAla 180  
QY 645 CCAGAGCTCTCGAGCAGAAACCTTACGGAAGCGTAGATGTGTGGCCCTCGGTGTGC 704  
Db 181 ProGluLeuLeuGluGlnLysProTyrGlyLysAlaValAspValTrpAlaLeuGlyVal 200  
QY 705 ATCTCTCATCTCTGTGTGGTACCCCTTCTATGATGAGAGCGATCCTGAACCTC 764  
Db 201 IleSerTyrIleLeuLeuCysGlyTyrProPheTyrAspGluSerAspProGluLeu 220  
QY 765 TTCAGCCGATTTCTGAGGCGCAGCTATGAGTTTGTACTCCCTTTTGGGATGACATCTCA 824  
Db 221 PheSerGlnIleLeuArgAlaSerTyrGluPheAsp\*\*\*ProPheTyrAspAspIleSer 240  
QY 825 GAATCAGCCAAAGACTTTCATTCGCCACCTTCTGGAACGTGATCCCCAGAGAGGTTCCAC 884  
Db 241 GluSerGlyLysAspPheIleArgHisLeuLeuGluArgAspLeuGlnLysArgPheThr 260  
QY 885 TGCCAGCAGCGCCTTACAGCATCTTTGGATCTCTGGGGATGCAGCCTTCGATAGGGACATC 944  
Db 261 CysGlnGlnAlaLeuArgAspLeuTrpIlePheTyrAspThrGlyPheGlyArgAspIle 280  
QY 945 CTGGGTTCTGTGATGAGCAGATCCAGAGAATTTTCCAGGACCCACCTGGAAGCCTGCA 1004  
Db 281 LeuGlyPheValSerGluGlnIleArgLysAsnPheAlaTrpThrHisTrpLysArgAla 300  
QY 1005 TTCAATGCCACATCATCTCTAGTCCATCGTAAAGCTGGGCAAAAGCCAGAGGTTGAG 1064  
Db 301 PheAsnAlaThrLeuPheLeuArgHisIleArgLysLeuGlyGlnIleProGluGlyGlu 320  
QY 1065 GAGGCTCTCAGGACGATGTATGACCCCTCATAGCCACCCAGGCTTGGGACTAGCCAGTCC 1124  
Db 321 GlyAlaSerGluGlnGlyMet\*\*\*ArgHisSerHis\*\*GlyLeuArgAlaGlyGlnPro 340  
QY 1125 CCCAAGTGG 1133  
Db 341 ProLysTrp 343  
RESULT 6  
ADL06509  
ID ADL06509 standard; protein; 343 AA.  
XX  
AC ADL06509;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Human tumour-associated antigenic target (TAT) polypeptide #8.  
XX  
KW Human; tumour-associated antigenic target; TAT; cell death; tumour;  
KW cancer; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN WO2004016225-A2.  
XX  
XX 26-FEB-2004.  
XX  
XX 19-AUG-2003; 2003WO-US025892.  
XX  
XX 19-AUG-2002; 2002US-0404809P.  
PR 21-AUG-2002; 2002US-0405645P.  
PR 23-SEP-2002; 2002US-0413192P.  
PR 15-OCT-2002; 2002US-0419008P.

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PR 15-NOV-2002; 2002US-0426847P.
PR 02-JUL-2003; 2003US-0484959P.
XX (GETH ) GENENTECH INC.
XX Desauvage FJ, Frantz G, Hillan KJ, Polakis P, Polson A, Smith V;
PI Spencer SD, Wu TD, Zhang Z;
DR N-PSDB; ADL06429.
XX WPI; 2004-257144/24.
XX
XX New antibody that binds to a tumor-associated antigenic target (TAT)
PT polypeptide, useful for preparing a composition for diagnosing or
PT treating cancer.
XX
XX Claim 2; SEQ ID NO 89; 319pp; English.
XX
XX The present invention relates to the isolation of human tumour-associated
CC antigenic target (TAT) polynucleotide and polypeptide sequences. Also
CC disclosed is an antibody that binds to a TAT polypeptide. The antibody is
CC a monoclonal antibody, an antibody fragment, a chimeric antibody or a
CC humanised antibody. It is conjugated to a growth inhibitory agent. It is
CC produced in bacteria or in CHO cells and induces death of a cell to which
CC it binds. The antibody is useful for preparing a composition for
CC diagnosing or treating tumours and cancer. The present sequence
CC represents a human TAT polypeptide of the invention.
XX
XX Sequence 343 AA;
SQ
Alignment Scores:
Pred. No.: 3,73e-126 Length: 343
Score: 1625.00 Matches: 316
Percent Similarity: 93.29% Conservative: 4
Best Local Similarity: 92.13% Mismatches: 23
Query Match: 56.58% Indels: 0
DB: 8 Gaps: 0
US-10-032-254A-1 (1-1554) x ADL06509 (1-343)
QY 105 ATGCTGCTGCTCAAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAG 164
DB 1 MetLeuLeuLeuLysHisThrGluAspIleSerValTyrGluIleArgGluArg 20
QY 165 CTGGGCTCGGGTGCCTCTCTCTGAGGTGATGCTGCGCCAGGAAAGGGGCTCTGCTCATCTT 224
DB 21 LeuGlySerGlyAlaPheSerGluValValLeuAlaGlnGluArgGlySerAlaHisLeu 40
QY 225 GTGGCCCTCAAGTGCATTTCCAAAGAAAGCATCTTCGGGGCAAGGAGCCCTGTGGAGAAAT 284
DB 41 ValAlaLeuLysCysIleProLysLysAlaLeuArgGlyLysGluAlaLeuValGluAsn 60
QY 285 GAGATCGCGGTACTTCGCAGAAATCCGCCATCCCAACATTTGGCTCTGGAGGAGCTCCAT 344
DB 61 GluIleAlaValLeuArgArgIleSerHisProAsnIleValAlaLeuGluAspValHis 80
QY 345 GAGAGTCTTCTCATCTCTACTTTGGCCATGCTGTACAGTGTGTGAACCTTTTGAC 404
DB 81 GluSerProSerHisLeuTyrLeuAlaMetGluLeuValThrGlyGluLeuPheAsp 100
QY 405 CGCATCATGAGCGGGGCTCCTTACACAGAGAAGAGCCAGCCACCTTGTAGGCGAGGTC 464
DB 101 ArgIleMetGluArgGlySerTyrThrGluLysAspAlaSerHisLeuValGlyGlnVal 120
QY 465 CTTGGGCTGCTCTCTACCTTCATAGCTGGGATGTGTCACCGGAGACCTCAAGCCTGAA 524
DB 121 LeuGlyAlaValSerTyrLeuHisSerLeuGlyIleValHisArgAspLeuLysProGlu 140
QY 525 AACCTCTCTATGCCACACCTTTTGGAGCTTCCAGATCATGTCTCTGACTTTGGCCTG 584
DB 141 AsnLeuLeuTyrAlaThrProPheGluAspSerLysIleMetValSerAspPheGlyLeu 160
QY 585 TCCAAAATACAGCTGGCAACATGCTAGGCACAGCCTGTGGGACCCCGAGGATATGTGGCC 644
DB 161 SerLysIleGlnAlaGlyAsnMetLeuGlyThrAlaCysGlyThrProGlyTyrValAla 180
QY 645 CCAGAGCTCTCTGAGCAGAAACCTACGAGGAGCGCTAGATGTGTGGGGCCCTGGGTGTC 704
DB 181 ProGluLeuLeuGluGlnLysProTyrGlyLysAlaValAspValTyrAlaLeuGlyVal 200
QY 705 ATCTCTCATATCTGCTGTGTGGGTACCCCTCTCTATGATGAGAGCGGATCTCTGAACCTC 764
DB 201 IleSerTyrIleLeuLeuCysGlyTyrProPheTyrAspGluSerAspProGluLeu 220
QY 765 TTCAGCCAGATTTCTGAGGCCAGCTATGATTTGACTCCCTCTTTGGGATGACATCTCA 824
DB 221 PheSerGlnIleLeuArgAlaSerTyrGluPheAsp***ProPheTyrAspAspIleSer 240
QY 825 GAATCAGCCAAAGACTTTCATTCGCCACCTTCTCTGAAACGTGATCCCCAGAGAGGTTCCACC 884
DB 241 GluSerGlyLysAspPheIleArgHisLeuLeuGluArgAspLeuGlnLysArgPheThr 260
QY 885 TGCAGCAGGCCCTACAGCATCTTTGGATCTCTGGGATGCGAGCCTTCGATAGGAGCATC 944
DB 261 CysGlnGlnAlaLeuArgAspLeuTyrPheTyrAspThrGlyPheGlyArgAspIle 280
QY 945 CTGGGTTCTCTCAGTCAGCAGATCCAGAGAAGATTTTCCAGGACCCACTCGAAGCCGTGCA 1004
DB 281 LeuGlyPheValSerGluGlnIleArgLysAsnPheAlaTyrThrHisTyrLysArgAla 300
QY 1005 TTCAATGCCACATCATTTCTACGTACATCCGTAAGCTGGGACAAAGCCAGAGGGTGAG 1064
DB 301 PheAsnAlaThrLeuPheLeuArgHisIleArgLysLeuGlyGlnIleProGluGlyGlu 320
QY 1065 GAGGCTTCAGGAGCAGTGTATGACCCCTCATAGCCACCCAGGCTTGGGACTAGCCAGTCC 1124
DB 321 GlyAlaSerGluGlnGlyMet***ArgHisSerHis***GlyLeuArgAlaGlyGlnPro 340
QY 1125 CCCAGCTGG 1133
DB 341 ProLysTyr 343
RESULT 7
ADM72655
ID ADM72655 standard; protein; 343 AA.
XX ADM72655;
XX 17-JUN-2004 (first entry)
XX Human TASK120 polypeptide (clone DNA151475).
XX TASK; tumour-associated kinase; cytostatic; tumour;
XX cell proliferative disorder; cancer; transgenic;
XX chromosome identification; tissue typing; human; TASK120; enzyme.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Misc-difference 233 /note= "encoded by TNT"
XX FT Misc-difference 328 /note= "encoded by GSC"
XX FT Misc-difference 333 /note= "encoded by TNA"
XX PN WO2004024063-A2.
XX 25-MAR-2004.
XX 05-SEP-2003; 2003WO-US027886.
XX 11-SEP-2002; 2002US-0410166P.
XX (GETH ) GENENTECH INC.
XX Davis DP, Desauvage FJ, Wood WI, Zhang Z;
```

XX WPI; 2004-282984/26.  
DR N-PSDB; ADM72654.  
XX  
PT New tumor-associated kinase nucleic acids and polypeptides, useful as  
PT hybridization probes for isolating full length TASK DNA, for generating  
PT transgenic animals, in chromosome identification, or for tissue typing.  
XX  
PS Claim 11; Fig 6; 140pp; English.  
XX  
CC The invention relates to tumour-associated kinase (TASK) polypeptides  
CC (II) and encoding polynucleotides. An antibody, oligopeptide (siRNA) or  
CC organic molecule that binds to (II) is useful for treating a mammal  
CC having a tumour comprising cells expressing (II). Antagonists of TASK are  
CC useful for treating or preventing a cell proliferative disorder (e.g.  
CC cancer) associated with increased expression or activity of (II). The  
CC TASK polynucleotides and polypeptides may be used as hybridization probes  
CC for isolating full length TASK DNA, for generating transgenic animals, in  
CC chromosome identification, or for tissue typing. The present sequence  
CC represents a human TASK120 polypeptide.  
XX  
SQ Sequence 343 AA;  
  
Alignment Scores:  
Pred. No.: 3,73e-126 Length: 343  
Score: 1625.00 Matches: 316  
Percent Similarity: 93.29% Conservative: 4  
Best Local Similarity: 92.13% Mismatches: 23  
Query Match: 56.58% Indels: 0  
DB: 8 Gaps: 0  
  
US-10-032-254A-1 (1-1554) x ADM72655 (1-343)  
  
QY 105 ATGCTGCTGCTCAAGAAACAGACGAGCATCAGCAGTGTCTATGAGATCCGGGAGAAG 164  
DB 1 MetLeuLeuLeuLysHisThrGluAspIleSerValTyrGluIleArgGluArg 20  
  
QY 165 CTGGGCTCGGGTCTTCTCTGAGGTGATGCTGGCCAGGAAAGGGGCTCTGCTCATCTT 224  
DB 21 LeuGlySerGlyAlaPheSerGluValValLeuAlaGlnGluArgGlySerAlaHisLeu 40  
  
QY 225 GTGGCCTCAGAGTCATCCCAAGAGCAGCTTCGGGGCAAGAGCCCTGTGGGAGAAT 284  
DB 41 ValAlaLeuLysCysIleProLysLysAlaLeuArgGlyLysGluAlaLeuValGluAsn 60  
  
QY 285 GAGATCCGCTACTTCCGAGAATCAGCCATCCCAATTTGCTGCTCTGGAGGACGTCAT 344  
DB 61 GluIleAlaValLeuArgAlaGlySerHisProAsnIleValAlaLeuGluAspValHis 80  
  
QY 345 GAGAGTCTTCTCATCTCTACTTGGCCATGAGCTGGTAACAGGTGTGAACTGTTTGAC 404  
DB 81 GluSerProSerHisLeuTyrLeuAlaMetGluLeuValThrGlyGlyGluLeuPheAsp 100  
  
QY 405 CGCATCATGAGGGGCTCTCACAGAGAAGAGCCAGCCAGCCCTGTAGGGCAGGTC 464  
DB 101 ArgIleMetGluArgGlySerTyrThrGluLysAspAlaSerHisLeuValGlyGlnVal 120  
  
QY 465 CTGGGCGCTCTCTACCTTCTATGCTGGGATCGTCACCGGACCTCAAGCCCTGAA 524  
DB 121 LeuGlyAlaValSerTyrLeuHisSerLeuGlyIleValHisArgAspLeuLysProGlu 140  
  
QY 525 AACTCTCTATGCCACACTTTGAGGACTCCAAAGATCATGCTCTCTGACTTTGGCGTG 584  
DB 141 AsnLeuLeuTyrAlaThrProPheGluAspSerLysIleMetValSerAspPheGlyLeu 160  
  
QY 585 TCCAAATACAGCTGCACATCTAGGACAGCCCTGTGGACCCCGAGGATATGTGCC 644  
DB 161 SerLysIleGlnAlaGlyAsnMetLeuGlyThrAlaCysGlyThrProGlyTyrValAla 180  
  
QY 645 CCAGAGCTCTGGAGCAGAAACCTTACGGGAAGCCGTAGATGTGTGGCCCTGGGTGTC 704  
DB 181 ProGluLeuLeuGluGlnLysProTyrGlyLysAlaValAspValTrpAlaLeuGlyVal 200

QY 705 ATCTCTACATCTCTGTGTGGGTACCCCTTCTATGATGAGAGCATCTCTGAATC 764  
DB 201 IleSerTyrIleLeuLeuLeuCysGlyTyrProPheTyrAspGluSerAspProGluLeu 220  
  
QY 765 TTCAGCCAGATTCTGAGGGCCAGCTATGAGTTTGACTCCCTTTTGGGATGACATCTCA 824  
DB 221 PheSerGlnIleLeuArgAlaSerTyrGluPheAsp\*\*\*ProPheTrpAspIleSer 240  
  
QY 825 GAATCAGCCAAAGACTTCATTCGCCACCTTCTGGAACTGATCCCGAAGAGGTTTACC 884  
DB 241 GluSerGlyLysAspPheIleArgHisLeuLeuGluArgAspLeuGlnLysArgPheThr 260  
  
QY 885 TCCAGAGCGCCCTACAGCATCTTTGGATCTCTGGGATGACGCTTCGATAGGGACATC 944  
DB 261 CysGlnGlnAlaLeuArgAspLeuTrpIlePheTrpAspThrGlyPheGlyArgAspIle 280  
  
QY 945 CTGGGTCTCTGTCAGTCAGCAGATCCAGAGAATTTTGCAGGACCCACCTGGAGCGTGCA 1004  
DB 281 LeuGlyPheValSerGluGlnIleArgLysAsnPheAlaTrpThrHisTrpLysArgAla 300  
  
QY 1005 TTCAATGCCACATCATTTCTACGTACATCCGTAAAGCTGGGACAAAGCCAGAGGGTGAG 1064  
DB 301 PheAsnAlaThrLeuPheLeuArgHisIleArgLysLeuGlyGlnIleProGluGlyGlu 320  
  
QY 1065 GAGGCTCCAGCAGTGTATGACCGCTCATGCCACCCAGCGCTTGGGACTAGCCAGTCC 1124  
DB 321 GlyAlaSerGluGlnGlyMet\*\*\*ArgHisSerHis\*\*\*GlyLeuArgAlaGlyGlnPro 340  
  
QY 1125 CCCAAGTGG 1133  
DB 341 ProLysTrp 343  
  
RESULT 8  
ADM72237  
ID ADM72237 standard; protein; 343 AA.  
XX  
AC ADM72237;  
XX  
DT 17-JUN-2004 (first entry)  
XX  
DE Human TASK100 polypeptide.  
XX  
KW TASK; tumour-associated kinase; cytostatic; tumour antigen;  
XX cell proliferative disorder; cancer; transgenic; human.  
OS Homo sapiens.  
XX  
PN WO2004024064-A2.  
XX  
PD 25-MAR-2004.  
XX  
PF 05-SEP-2003; 2003WO-US027894.  
XX  
PR 11-SEP-2002; 2002US-0410166P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Desauvage FJ, Wood WI, Zhang Z;  
XX  
DR WPI; 2004-282985/26.  
DR N-PSDB; ADM72236.  
XX  
PT New tumor-associated kinase nucleic acids and polypeptides, useful as  
PT hybridization probes for isolating full length TASK DNA, for generating  
PT transgenic animals, in chromosome identification, or for tissue typing.  
XX  
PS Claim 12; SEQ ID NO 42; 163pp; English.  
XX  
CC The invention relates to new isolated tumour-associated kinase (TASK)  
CC nucleic acid molecules and encoded polypeptides. Cytostatic. The  
CC antibody, oligopeptide or organic molecule that binds to the TASK  
CC polypeptide are useful for treating a mammal having a tumour comprising  
CC cells expressing the polypeptide. Antagonists of TASK are useful for

CC treating or preventing a cell proliferative disorder (e.g. cancer)  
CC associated with increased expression or activity of TASK polypeptide. The  
CC TASK polynucleotides and polypeptides may be used as hybridization probes  
CC for isolating full length TASK DNA, for generating transgenic animals, in  
CC chromosome identification, or for tissue typing. The present sequence  
CC represents a human TASK polypeptide.  
XX  
SQ Sequence 343 AA;

## Alignment Scores:

Pred. No.: 3,73e-126 Length: 343  
Score: 1625.00 Matches: 316  
Percent Similarity: 93.29% Conservative: 4  
Best Local Similarity: 92.13% Mismatches: 23  
Query Match: 56.58% Indels: 0  
DB: 8 Gaps: 0

US-10-032-254A-1 (1-1554) x ADM72237 (1-343)

QY 105 ATGCTCTGCTCAAGAAACAGACGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAG 164  
Db 1 MetLeuLeuLeuLysHisThrGluAspIleSerSerValTyrGluIleArgGluArg 20  
QY 165 CTGGGCTCGGCTCTCTCTGAGGTGATGCTGGCCAGAAAGGGCTCTGCTCATCTT 224  
Db 21 LeuGlySerGlyAlaPheSerGluValValLeuAlaGlnGluArgGlySerAlaHisLeu 40  
QY 225 GTGGCCCTCAAGTGCATTCCTCAAGAAAGCACTTCGGGGCAAGGAGCCCTGTGGAGAAT 284  
Db 41 ValAlaLeuLysCysIleProLysLysAlaLeuArgGlyLysGluAlaLeuValGluAsn 60  
QY 285 GAGATCCGGTACTTCGCAAGATCAGCCATCCCAACATTGTGCTCTGGAGGACGTCAT 344  
Db 61 GluIleAlaValLeuArgIleSerHisProAsnIleValAlaLeuGluAspValHis 80  
QY 345 GAGAGTCTCTCATCTCTACTTGGCCATGAGCTGGTAACAGTGGTGAACCTGTTGAC 404  
Db 81 GluSerProSerHisLeuTyrLeuAlaMetGluLeuValThrGlyGlyGluLeuPheAsp 100  
QY 405 CGCATCATGAGGGGGCTCTACACAGAGAAGAGCCAGCCACCTTGTAGGGCAGGTC 464  
Db 101 ArgIleMetGluArgGlySerThrGluLysAspAlaSerHisLeuValGlyGlnVal 120  
QY 465 CTGGCGCTCTCTCTACCTTCATAGCCTGGGATCGTCACCGGACCTCAAGCCTGAA 524  
Db 121 LeuGlyAlaValSerTyrLeuHisSerLeuGlyIleValHisArgAspLeuLysProGlu 140  
QY 525 AACCTCTCTATGCCACACTTTTGGAGTCCCAAGATCATGCTCTGACTTTGGCCTG 584  
Db 141 AsnLeuLeuTyrAlaThrProPheGluAspSerLysIleMetValSerAspPheGlyLeu 160  
QY 585 TCCAAATACAGCTGGCAACATGCTAGGCACAGCCTGTGGACCCCGAGATATGTGCC 644  
Db 161 SerLysIleGlnAlaGlyAsnMetLeuGlyThrAlaCysGlyThrProGlyTyrValAla 180  
QY 645 CCAGAGCTCTCTGAGCAGAAACCTTACGGAGGCGCTAGATGTGGGCGCTGGGTGTC 704  
Db 181 ProGluLeuLeuGluGlnLysProTyrGlyLysAlaValAspValTrpAlaLeuGlyVal 200  
QY 705 ATCTCTACATCTCTGTGTGGGTACCCCTTCTATGATGAGACGATCTCTGAATC 764  
Db 201 IleSerTyrIleLeuLeuCysGlyTyrProPheTyrAspGluSerAspProGluLeu 220  
QY 765 TTCAGCCAGATTCGTGGGCGCAGCTAGTGTGACTCCCTTTGGGATGACATCTCA 824  
Db 221 PheSerGlnIleLeuArgAlaSerTyrGluPheAsp\*\*\*ProHtrpAspAspIleSer 240  
QY 825 GAATCAGCAAGACTTCTTCGCCACCTTCTGGAAGCTGATCCCGAAGAGGTTCAAC 884  
Db 241 GluSerGlyLysAspPheIleArgHisLeuLeuGluArgAspLeuGlnLysArgPheThr 260  
QY 885 TGCAGCAGGCGCTACAGCATCTTTGGATCTCTGGGGGATGACGCTTCGATAGGACATC 944  
|||||

Db 261 CysGlnGlnAlaLeuArgAspLeuTrpIlePheTrpAspThrGlyPheGlyArgAspIle 280  
QY 945 CTGGGTCTCTGTCAGTCAGCAGATCCAGAAAGATTTTCCAGGACCCACCTGGAAGCGTGCA 1004  
Db 281 LeuGlyPheValSerGluGlnIleArgLysAsnPheAlaTrpThrHisTrpLysArgAla 300  
QY 1005 TTCAATGCCACATCATCTCTAGCTACATCCGTAACTGGGACAAAGCCAGAGGTGAG 1064  
Db 301 PheAsnAlaThrLeuPheLeuArgHisIleArgLysLeuGlyGlnIleProGluGlyGlu 320  
QY 1065 GAGGCTCTCAGGCGAGTGTATGACCCCTCATAGCACCAGGCTCTGGGACTAGCCAGTCC 1124  
Db 321 GlyAlaSerGluGlnGlyMet\*\*\*ArgHisSerHis\*\*\*GlyLeuArgAlaGlyGlnPro 340  
QY 1125 CCCAAGTGG 1133  
Db 341 ProLysTrp 343  
RESULT 9  
ID ABR41269 standard; protein; 270 AA.  
XX ABR41269;  
AC ABR41269;  
XX 02-JUN-2003 (first entry)  
DT Human DITHP intracellular signalling protein.  
DE  
XX Human: dithp; diagnostic and therapeutic polynucleotide; diagnosis;  
KW cancer; cell proliferative disorder; autoimmune disorder;  
KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;  
KW neurological disorder; gastrointestinal disorder; transport disorder;  
KW connective tissue disorder; drug screening; proteome analysis;  
KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;  
KW disease model; toxicological testing; transcript imaging;  
KW intracellular signalling.  
XX  
XX Homo sapiens.  
XX WO200297031-A2.  
XX 05-DEC-2002.  
PD  
XX 27-MAR-2002; 2002WO-US010056.  
PF  
XX 28-MAR-2001; 2001US-0279619P.  
PR  
XX 29-MAR-2001; 2001US-0280067P.  
PR  
XX 29-MAR-2001; 2001US-0280068P.  
PR  
XX 16-MAY-2001; 2001US-0291280P.  
PR  
XX 17-MAY-2001; 2001US-0291829P.  
PR  
XX 17-MAY-2001; 2001US-0291849P.  
PR  
XX 19-JUN-2001; 2001US-0299428P.  
PR  
XX 20-JUN-2001; 2001US-0299776P.  
PR  
XX 20-JUN-2001; 2001US-0300001P.  
XX  
(INCY-) INCYTE GENOMICS INC.  
XX Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;  
XX Dufour GE, Hillman JR, Yu JY, Tuason O, Yap PE, Ameshey SR;  
XX Baugthery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;  
XX Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;  
XX Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;  
XX WPI; 2003-129518/12.  
DR N-PSDB; ACC46211.  
XX  
PT Novel human diagnostic and therapeutic polypeptide useful for identifying  
PT test compound which specifically binds to a polypeptide encoded by human  
PT diagnostic and therapeutic polynucleotide, and to induce antibodies.  
XX  
PS Claim 27; SEQ ID NO 804; 591pp; English.  
XX  
CC The invention relates to novel human diagnostic and therapeutic

CC polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded  
CC proteins (DITHP; ABR41136-ABR41812). The invention also relates to  
CC polynucleotide sequences at least 90% identical to the dithp cDNA  
CC sequences of the invention; recombinant vectors, host cells and  
CC transgenic organisms comprising a dithp nucleic acid sequence; the  
CC recombinant production of DITHP proteins; antibodies specific for DITHP  
CC proteins; microarrays comprising dithp nucleic acid sequences; methods of  
CC detecting dithp nucleotide and protein sequences; methods of screening  
CC for compounds which specifically bind a DITHP protein; and methods of  
CC assessing the toxicity of test compounds using a dithp hybridisation  
CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the  
CC diagnosis of a wide variety of conditions including cancer and other cell  
CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,  
CC viral, fungal or parasitic infections; hormonal disorders; metabolic  
CC disorders; neurological disorders; gastrointestinal disorders; transport  
CC disorders; and connective tissue disorders. They may also be used to  
CC screen for modulators of protein activity or gene expression. DITHP  
CC proteins can additionally be used in analysis of the proteome of a tissue  
CC or cell type and to induce antibodies. The dithp nucleic acids are  
CC additionally useful in somatic or germline gene therapy of the disorders  
CC mentioned above, as a source of antisense sequences, as a source of  
CC probes and primers, in genotyping and identification of individuals, in  
CC the generation of transgenic animal models of human disease or knock in  
CC humanised animals, in toxicological testing, and in transcript imaging.  
CC The present sequence represents a DITHP protein which has intracellular  
CC signalling activity. Note: The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 270 AA;

Alignment Scores:  
Pred. No.: 9,65e-96 Length: 270  
Score: 1259.00 Matches: 238  
Percent Similarity: 95.62% Conservative: 2  
Best Local Similarity: 94.82% Mismatches: 11  
Query Match: 43.84% Indels: 0  
DB: 6 Gaps: 0

US-10-032-254A-1 (1-1554) x ABR41269 (1-270)

QY 381 GTACAGGTCGTGACCTGTTGACCCGATCATGGAGCGGGCTCTACACAGAGAGGAC 440  
DB 20 ValThrGlyGluLeuPheAspArgileMetGluArgGlySerTyrThrGluLysAsp 39  
QY 441 GCCAGCCACCTTGTAGGCGCAGGTCCTTGGCGCTGTCTCTACCTTCATAGCCTGGGCATC 500  
DB 40 AlaSerHisLeuValGlyGlnValLeuGlyAlaValSerTyrLeuHisSerLeuGlyIle 59  
QY 501 GTGCACGGGACCTCAAGCCTGAAACCTCTCTATGCCACACCTTTTGAGGACTCCAAG 560  
DB 60 ValHisArgAspLeuLysProGluAsnLeuTyrAlaThrProPheGluAspSerLys 79  
QY 561 ATCATGGTCTCTGACTTTGGCTGTCCAAATACAGCTGCGCAACATGCTAGCACAGCC 620  
DB 80 IleMetValSerAspPheGlyLeuSerLysIleGlnAlaGlyAsnMetLeuGlyThrAla 99  
QY 621 TGTGGGACCCAGGATATGGCCCCAGAGCTCTCGAGCAGAGAAACCTTACGGGAAGGCC 680  
DB 100 CysGlyThrProGlyTyrValAlaProGluLeuLeuGluGlnLysProTyrGlyLysAla 119  
QY 681 GTAGATGTGGGCGCTGGGTGTCTATCTCTACATCTGTGTGGGTATCCGCCCTTC 740  
DB 120 ValAspValThrAlaLeuGlyValIleSerTyrIleLeuLeuCysGlyTyrProProPhe 139  
QY 741 TATCATGACCGCATCTGTAACCTTTCAGCAGATCTTCTAGGCGCCAGCTATGATTTGAC 800  
DB 140 TyrAspGluSerAspProGluLeuPheSerGlnIleLeuArgAlaSerTyrGluPheAsp 159  
QY 801 TCCCGCTTTTGGGATGACATCTCAGAATCAGCCAAAGACTTCATTCGCCACCTTCTGGAA 860  
DB 160 SerProPheThrAspAspIleSerGluSerAlaLysAspPheIleArgHisLeuLeuGlu 179

QY 861 CGTGATCCCCAGAGAGGTTTACCTGCCAGCAGGCGCTACAGCATCTTTGGGATCTCTGGG 920  
DB 180 ArgAspProGlnLysArgPheThrCysGlnGlnAlaLeuArgHisLeuTrpIleSerGly 199  
QY 921 GATGAGCCTTCGATAGGACATCTCGGTTCTGTCTAGTGACAGATCCAGAAATTTT 980  
DB 200 AspThrAlaPheAspArgAspIleLeuGlySerValSerGluGlnIleArgLysAsnPhe 219  
QY 981 GCAGAGCCCATCGAAGGCTGCATTCATGCCATCATCTTCTAGCTCACATCCGTAAG 1040  
DB 220 AlaArgThrHisTrpLysArgAlaPheAsnAlaThrSerPheLeuArgHisIleArgLys 239  
QY 1041 CTGGGACAAAGCCGAGGCTGAGGAGGCTCCAGGCACTGTATGACCTCATAGCCAC 1100  
DB 240 LeuGlyGlnIleProGluGlyGluGlyAlaSerGluGlnGlyMetAlaArgHisSerHis 259  
QY 1101 CCAGGCTTTGGGACTAGCCAGTCCCGCCCAAGTGG 1133  
DB 260 SerGlyLeuArgAlaGlyGlnProProlysTrp 270  
RESULT 10  
ABR41299  
ID ABR41299 standard; protein; 250 AA.  
XX  
AC ABR41299;  
XX  
DT 02-JUN-2003 (first entry)  
XX  
DE Human DITHP intracellular signalling protein.  
XX  
KW Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;  
KW cancer; cell proliferative disorder; autoimmune disorder;  
KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;  
KW neurological disorder; gastrointestinal disorder; transport disorder;  
KW connective tissue disorder; drug screening; proteome analysis;  
KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;  
KW disease model; toxicological testing; transcript imaging;  
KW intracellular signalling.  
XX  
OS Homo sapiens.  
XX  
PN WO200297031-A2.  
XX  
PD 05-DEC-2002.  
XX  
PF 27-MAR-2002; 2002WO-US010056.  
XX  
PR 28-MAR-2001; 2001US-0279619P.  
PR 29-MAR-2001; 2001US-0280067P.  
PR 29-MAR-2001; 2001US-0280068P.  
PR 16-MAY-2001; 2001US-0291280P.  
PR 17-MAY-2001; 2001US-0291829P.  
PR 17-MAY-2001; 2001US-0291849P.  
PR 19-JUN-2001; 2001US-0299428P.  
PR 20-JUN-2001; 2001US-0299776P.  
PR 20-JUN-2001; 2001US-0300001P.  
XX  
PA (INCY-) INCYTE GENOMICS INC.  
XX  
PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;  
PI Daffour GE, Hillman JR, Yu JY, Tuason O, Yap PE, Anshey SR;  
PI Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;  
PI Peralta CH, David MH, Lewis SA, Chen AD, Panzer SR, Harris B;  
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;  
XX  
DR WPI: 2003-129518/12.  
DR N-PSDB; ACC46241.  
XX  
PT Novel human diagnostic and therapeutic polypeptide useful for identifying  
PT test compound which specifically binds to a polypeptide encoded by human  
PT diagnostic and therapeutic polynucleotide, and to induce antibodies.  
XX  
PS Claim 27; SEQ ID NO 834; 591pp; English.





CC cells and rapidly moves to the cytoplasm on activation by the kinases  
 CC p38/p40/RK. While in the nucleus, MAPKAPK2 contributes to the  
 CC phosphorylation of CREB (cAMP response element-binding protein), and is  
 CC also responsible for phosphorylating serum response factor and the  
 CC transcription factor E47. In the cytoplasm, MAPKAPK2 phosphorylates the  
 CC small heat shock protein HSP25/HSP27, lymphocyte specific protein (LSP1),  
 CC glycogen synthase, tyrosine hydroxylase (the rate-limiting enzyme in  
 CC catecholamine synthesis) and 5-lipoxygenase, a key enzyme in leukotriene  
 CC biosynthesis. Mice which lack MAPKAPK2 show increased stress resistance  
 CC and survive bacterial LPS-induced endotoxemic shock due to a 90% reduction  
 CC in the production of TNF-alpha. The crystal structure of MAPKAPK2 may be  
 CC used to evaluate the ability of a chemical entity to interact with  
 CC binding pockets or other key domains of MAPKAPK2, and in rational drug  
 CC design. MAPKAPK2-specific agonists and antagonists identified using the  
 CC crystal structure may be used in the treatment of disorders related to  
 CC MAPKAPK2. The present sequence represents calcium/calmodulin-dependent  
 CC protein kinase I (CamKI), a homologue of MAPKAPK2.  
 XX  
 SQ Sequence 332 AA;

Alignment Scores:  
 Pred. No.: 1,64e-89 Length: 332  
 Score: 1184.50 Matches: 220  
 Percent Similarity: 85.17% Conservative: 50  
 Best Local Similarity: 69.40% Mismatches: 44  
 Query Match: 41.24% Indels: 3  
 DB: 7 Gaps: 2

US-10-032-254A-1 (1-1554) x ADC15044 (1-332)

QY 120 AATCGAGCGAGGACATCAGCATGCTATGATCGGGAGAGTGGGCTCGGTGCC 179  
 DB 11 LysGlnAlaGluAspIleArgAspIleTyrAspPheArgValLeuGlyThrGlyAla 30  
 QY 180 TTCTCTGAGTGATGCTGGCCAGGAAAGGGCTCTGCTCATCTTGTGGCCCTCAAGTGC 239  
 DB 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50  
 QY 240 ATTCCCAAGAACACTTCCGGGCAAGAGGCCCTGGTGAGAAATGAGATCGCGGTACTT 299  
 DB 51 IleAlaLysLysAlaLeuGluGlyLysGluGlySerMetGluAsnGluIleAlaValLeu 70  
 QY 300 CGCAGAGATCAGCATCCCAACATTTGGCTCTGGAGGACGCTCCATGAGAGTCTTCTCAT 359  
 DB 71 HisLysIleLysHisProAsnIleValAlaLeuAspIleTyrGluSerGlyGlyHis 90  
 QY 360 CTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTGTTGACCGCATCATGGAGCGG 419  
 DB 91 LeuTyrLeuIleMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGluLys 110  
 QY 420 GGCTCTTACACAGAAAGGAGCCAGCACCTTTGTAGGGAGGTCTTGGCGCTGTCTCC 479  
 DB 111 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130  
 QY 480 TACTTTCATAGCTGGGCTGCTGCACGGGACCTCAAGCTGAAACCTCTCTATGCC 539  
 DB 131 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuLeuTyr 150  
 QY 540 ACACCTTTTGGAGACTCCAAAGATCATGCTCTGACATTTGGCTGTCCAAATACAA--- 596  
 DB 151 SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp 170  
 QY 597 GCTGGCAACATGCTAGGACAGCTGTGGGACCCAGGATATGTGGCCCGCAGAGCTCTG 656  
 DB 171 ProGlySerValLeuSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeu 190  
 QY 657 GAGCAGAAACCTTACGGGAGGCGGTAGATGTGGGCCCTGGTGTCTCTCATC 716  
 DB 191 AlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyrIle 210  
 QY 717 CTGCTGTGTGGTACCCCTCTCTATGATGAGAGCGATCTGAACTCTTCTCAGCCAGATT 776  
 DB 211 LeuLeuCysGlyTyrProProPheTyrAspGluAsnAspAlaLysLeuPheGluGlnIle 230

QY 777 CTGAGGCGCAGCTATGAGTTTCTGATCCCTTTTGGATGACATCTCAGAATCAGCAAA 836  
 DB 231 LeuLysAlaGluTyrGluPheAspSerProTyrTrpAspIleSerAspSerAlaLys 250  
 QY 837 GACTTTCATTCGCCACCTCTCTGGAACGTGATCCCGAAGAGGTTCACCTGCCAGAGGCC 896  
 DB 251 AspPheIleArgHisLeuMetGluLysAspProGluLysArgPheThrCysGluGlnAla 270  
 QY 897 CTACAGCATCTTGGATCTCTGGGATGAGCCTTCGATAGGACATCTCGGTCTCTGTC 956  
 DB 271 LeuGlnHisProTrpIleAlaGlyAspThrAlaLeuAspLysAsnIleHisGlnSerVal 290  
 QY 957 ACTGAGCAGATCCAGAGAATTTTCCAGAGCCCACTGGAAGCGTGCATTCAATGCCACA 1016  
 DB 291 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 310  
 QY 1017 TCATTCTACGTACATCCGTAAG-----CTGGGACAAAGCCAGAGGT 1061  
 DB 311 AlaValValArgHisMetArgLysLeuGlnLeuGlyHisGlnProGlyGly 327  
 RESULT 12  
 AAE34492  
 ID AAE34492 standard; protein; 370 AA.  
 XX  
 AC AAE34492;  
 XX  
 DT 14-MAY-2003 (first entry)  
 XX  
 DE Human camKI protein.  
 XX  
 KW Human; pyridylpyrimidine derivative; cellular protein kinase; Scrapie;  
 KW cellular protein phosphatase; cellular signal transduction; prophylaxis;  
 KW prion infection; chronic wasting disease; CWD; Creutzfeldt-Jacob disease;  
 KW CJD; transmissible mink encephalopathy; bovine spongiform encephalopathy;  
 KW TME; BSE; Gerstmann-Strausler-Scheinker syndrome; GSS; Alpers syndrome;  
 KW fatal familial insomnia; FFI; kuru; neurodegenerative disease; neurotic;  
 KW Alzheimer's disease; CamKI.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200293164-A2.  
 XX  
 PD 21-NOV-2002.  
 XX  
 PF 16-MAY-2002; 2002WO-BP005420.  
 XX  
 PR 16-MAY-2001; 2001EP-00111858.  
 PR 29-MAY-2001; 2001US-0293528P.  
 PR 13-JUL-2001; 2001EP-00117113.  
 PR 18-JUL-2001; 2001US-0305898P.  
 XX  
 PA (AXXI-) AXXIMA PHARM AG.  
 XX  
 PI Stein-Gerlach M, Salassidis K, Bacher G, Mueller S;  
 XX  
 DR WPI; 2003-120714/11.  
 DR N-PSDB; AAD52784.  
 XX  
 PT New pyridylpyrimidine derivatives useful in the treatment or prevention  
 PT of infectious disease e.g. Kuru syndrome and Creutzfeldt-Jacob disease  
 PT (CJD).  
 XX  
 PS Disclosure; Page 77-79; 96pp; English.  
 XX  
 CC The invention relates to novel pyridylpyrimidine derivatives and methods  
 CC of detecting prion infections and/or prion disease in an individual or in  
 CC cells, cell cultures and/or cell lysates. The method involves adding at  
 CC least one monoclonal or polyclonal antibody, oligonucleotide or pyridyl-  
 CC pyrimidine derivative to the sample or in cells, cell cultures and/or  
 CC cell lysates and detecting the activity of at least one human cellular  
 CC protein kinases (e.g., FGF-R1 (also known as flg, Flt-1, Flt-2, b-FGFR),  
 CC Tkt (also known as CCK-2, DDR-2 or EDDR; EC number 2.7.1.112), Abl (also



CC known as c-abl), ckl1, MKK7 (also known as SAPK1a, SAPKalpha), CDC2 (also known as CDK1), PRK), human cellular protein phosphatases such as PTP-SL (also known as MCP93) and PTP-zeta, the cellular signal transduction molecules HSP90 and GPR1-1. The invention is useful for regulating the production of prions in cells and in the manufacture of pharmaceutical composition for prophylaxis and/or treatment of infectious disease (e.g. Scrapie, chronic wasting disease (CWD), transmissible mink encephalopathy (TME), Creutzfeldt-Jacob disease (CJD), bovine spongiform encephalopathy (BSE), variant CJD, Gerstmann-Strausler-Scheinker syndrome (GSS), fatal familial insomnia (FFI), Kuru and Alpers syndrome, especially BSE, CJD, vCJD) or neurodegenerative diseases (e.g., Alzheimer's disease) in humans or ruminants. The present sequence is human cdk1 protein used in the invention

XX  
SQ Sequence 370 AA;

Alignment Scores:  
Pred. No.: 1.7e-89 Length: 370  
Score: 1184.50 Matches: 220  
Percent Similarity: 85.53% Conservative: 52  
Best Local Similarity: 69.18% Mismatches: 43  
Query Match: 41.24% Indels: 3  
DB: 6 Gaps: 2

US-10-032-254A-1 (1-1554) x AAB34492 (1-370)

QY 120 AAACAGAGGAGGACATCAGCAGTGTCTATGATCGGAGAGCTGGGCTCGGTGCC 179  
DB 11 LysGlnAlaGluAspIleArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla 30  
QY 180 TTCTCTGAGTGATGCTGGCCAGGAAAGGGCTCTGCTCATCTTGTGGCCCTCAAGTGC 239  
DB 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50  
QY 240 ATTCCCAAGAACACTTCGGGCAAGAGGCGCTGTGGAGATGAGTCGGGTACTT 299  
DB 51 IleAlaLysGluAlaLeuGlyLysGluGlySerMetGluAsnGluIleAlaValLeu 70  
QY 300 CGCAGATCAGCCATCCCAACATTTGGCTGTGGAGCAGCTCCATGAGATGCTCTCTCAT 359  
DB 71 HisLysIleLysHisProAsnIleValAlaLeuAspIleTyrGluSerGlyGlyHis 90  
QY 360 CTCTACTTGGCCATGGAGCTGGTAACAGTGGTGAACCTTTGACCGCATCATCGAGCGG 419  
DB 91 LeuTyrLeuIleMetGlnLeuValSerGlyGlyLeuPheAspArgIleValGluLys 110  
QY 420 GGCTCTACACAGAGAGGAGCCAGCCACCTTGTAGGCGAGTCTTGGCGCTGTCTCC 479  
DB 111 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130  
QY 480 TACCTTCATAGCTGGGCATCGTGCACCGGACCTCAAGCTGAAACCTCTCTATGCC 539  
DB 131 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuLeuTyr 150  
QY 540 ACACCTTTTGAGGACTCCAAAGATCATGCTCTGACTTTTGGCTGTGCAAAATACAA-- 596  
DB 151 SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp 170  
QY 597 GCTGGCAACATGTAGCAGCAGCTGTGGACCCAGGATATGTGGCCCGCAGAGCTCTG 656  
DB 171 ProGlySerValLeuSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeu 190  
QY 657 GAGCAGAAACCTTACGGAGGCGGTAGATGTGTGGCCCTGGGTGTCTCTCATATC 716  
DB 191 AlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyrIle 210  
QY 717 CTGCTGTGTGGGTACCCCTCTCTATGATCAGAGCATCTCTGAACCTCTTTCAGCCAGATT 776  
DB 211 LeuLeuCysGlyTyrProProPheTyrAspGluAsnAspAlaLysLeuPheGluGlnIle 230  
QY 777 CTGAGGCGCAGCTATGAGTTGATCCCTCTTTGGGATGACATCTCAGAAATCAGCCAAA 836  
DB 231 LeuLysAlaGluTyrGluPheAspSerProTyrTrpAspAspIleSerAspSerAlaLys 250

QY 837 GACTTCATTCGCCACCTTCTGGAACGTGATCCCAAGAGGTTCACTCCAGCAGGCC 896  
DB 251 AspPheIleArgHisLeuMetGluLysAspProGluLysArgPheThrCysGluGlnAla 270  
QY 897 CTACAGCATCTTTGGATCTCTGGGATCGAGCCTCGATAGGAGACATCTCGGTCTGTC 956  
DB 271 LeuGlnHisProTrpIleAlaGlyAspThrAlaLeuAspLysAsnIleHisGlnSerVal 290  
QY 957 AGTGAGCAGATCCAGAAAGAAATTTGCCAGGAGCCACCTGGAAGCGTGATTCATCAATGCCACA 1016  
DB 291 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 310  
QY 1017 TCATCTCTACGTCCATCCGTAAG-----CTGGACAAAGCCAGAGGTGAG 1064  
DB 311 AlaValValArgHisMetArgLysLeuGlnLeuGlyThrSerGlnGluGlyGln 328

#### RESULT 13

ADH23304  
ID ADH23304 standard; protein; 370 AA.

XX  
AC ADH23304;

XX  
DT 11-MAR-2004 (first entry)

XX  
DE Human calmodulin dependent protein kinase I.

XX  
KW human; kinase; kinase associated disorder; enzyme.

XX  
OS Homo sapiens.

XX  
PN US2003175926-A1.

XX  
PD 18-SEP-2003.

XX  
PF 05-MAR-2002; 2002US-00090002.

XX  
PR 05-MAR-2002; 2002US-00090002.

XX  
PA (PEKE ) PE CORP NY.

XX  
PI Yan C, Gong F;

XX  
DR WPI; 2004-119185/12.

XX  
PT A new isolated peptide related to the calcium/calmodulin-dependent protein kinase subfamily is useful to diagnose disorders and identify a compounds useful to treat disorders associated with expression of a kinase gene.

XX  
PS Disclosure; SEQ ID NO 4; 45pp; English.

XX  
CC The invention relates to a novel human kinase. The invention is useful for probes, primers, chemical intermediates, in biological assays, and transgenic non-human animals, to diagnose disorders involving an increase or decrease in kinase protein expression, and to identify a compound that can be used to treat a disorder associated with expression of a kinase gene. The present sequence represents the amino acid sequence of a human calmodulin dependent protein kinase I.

XX  
SQ Sequence 370 AA;

Alignment Scores:  
Pred. No.: 1.7e-89 Length: 370  
Score: 1184.50 Matches: 220  
Percent Similarity: 85.53% Conservative: 52  
Best Local Similarity: 69.18% Mismatches: 43  
Query Match: 41.24% Indels: 3  
DB: 6 Gaps: 2

US-10-032-254A-1 (1-1554) x ADH23304 (1-370)

QY 120 AAACAGAGGAGGACATCAGCAGTGTCTATGATCGGAGAGCTGGGCTCGGTGCC 179

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Db 11 LysGlnAlaGluAspIleArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla 30
Qy 180 TTCTCTGAGGTGATGCTGGCCAGGAAGGGCTCTGCTCATCTTGTGGCCCTCAAGTGC 239
Db 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50
Qy 240 ATTCCCAAGAAACACTTCGGGCGAAGGAGCCCTGGTGGAGATGAGATCGGGTACTT 299
Db 51 IleAlaLysGluAlaLeuGluGlyLysGluGlySerMetGluAsnGluIleAlaValLeu 70
Qy 300 CGCAGATCAGCCATCCCACTTGGCTCTGAGGAGCTCCATGAGATCTCTCAT 359
Db 71 HisLysIleLysHisProAsnIleValAlaLeuAspIleTyrGluSerGlyGlyHis 90
Qy 360 CTCTACTTGGCCATGGAGCTGTAACAGAGTGTCGAACTGTTTACCGCATCATGAGCGG 419
Db 91 LeuTyrLeuIleMetGlnLeuValSerGlyGluLeuPheAspArgIleValGluLys 110
Qy 420 GGCTCTTACACAGAAAGGAGCCGACCTTGTAGGGCAGGTCTTGGCGCTGTCTCC 479
Db 111 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130
Qy 480 TACTCTCATAGCTGGGCATCGTCACCGGACCTCAAGCTCAAACTCTCTCATGCC 539
Db 131 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuLeuTyr 150
Qy 540 ACACCTTTTGGAGACTCCAAAGATCATGCTCTGACTTTTGGCTTCCAAATACAA-- 596
Db 151 SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp 170
Qy 597 GCTGGCAACATGCTAGGCAAGCTGTGGGACCCAGGATATGTGGCCCGCAGAGCTCTG 656
Db 171 ProGlySerValLeuSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeu 190
Qy 657 GAGCAGAAACCTACGGAGGAGCGTAGATGTGGGCCCTGGGTGTCATCTCTCATC 716
Db 191 AlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyrIle 210
Qy 717 CTGCTGTGTGGTACCCCTCTTATGATGAGAGCGATCTGAACTCTTTCAGCCAGATT 776
Db 211 LeuLeuCysGlyTyrProPheTyrAspGluAsnAspAlaLysLeuPheGluGlnIle 230
Qy 777 CTGAGGCCAGCTATGATTTGATCCCTCTTGGGATGACATCTCAGAAATCAGCCAAA 836
Db 231 LeuLysAlaGluTyrGluPheAspSerProTyrTrpAspIleSerAspSerAlaLys 250
Qy 837 GACTTCATTCCCACTTCTGGAACGTATCCCGAGAGAGGTTCACCTGCCAGGCC 896
Db 251 AspPheIleArgHisLeuMetGluLysAspProGluLysArgPheThrCysGluGlnAla 270
Qy 897 CTACAGCATCTTTGGATCTCTGGGGATCGACGCTTCGATAGGAGACATCTGGTCTGTC 956
Db 271 LeuGlnHisProTyrIleAlaGlyAspThrAlaLeuAspLysAsnIleHisGlnSerVal 290
Qy 957 AGTGAGCAGATCCAGAAATTTTGGCAGGACCCACTGGAGCGCTGATTCATTCAGCACA 1016
Db 291 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 310
Qy 1017 TCATTCTACCTCATCCCTGAAG-----CTGGGACAAAGCCCGAGGGGTGAG 1064
Db 311 AlaValValArgHisMetArgLysLeuGlnLeuGlyThrSerGlnGluGlyGln 328
RESULT 14
ADL97820 standard; protein; 370 AA.
XX ADL97820;
AC ADL97820;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human CAMKI protein SeqID 6.
XX
```

```
KW human; neuropsychiatric disorder; bipolar disorder; schizophrenia;
KW alpha-type II calcium/calmodulin dependent protein kinase; CAMKII-alpha;
KW TBR1; Brachyury; neuroleptic; antidepressant; gene therapy;
KW mental disorder; mood disorder; psychosis; major depression; CAMKI.
XX
XX Homo sapiens.
XX
XX WO2004020455-A2.
XX
XX 11-MAR-2004.
XX
XX 26-AUG-2003; 2003WO-US026873.
XX
XX 28-AUG-2002; 2002US-0406879P.
XX
XX 27-FEB-2003; 2003US-0451306P.
XX
XX (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
XX Bunney WR, Jones EG, Molnar M;
XX
XX WPI; 2004-239152/22.
XX
XX N-PSDB; ADL97819.
XX
XX Determining whether a subject has or is predisposed to a mental disorder,
XX comprises detecting the level of reagent that selectively associates with
XX a specified polynucleotide or polypeptide in a sample from the subject.
XX
XX Disclosure; SEQ ID NO 6; 85pp; English.
XX
XX This invention relates to a novel method to determine whether a subject
XX has or is predisposed to a mental or neuropsychiatric disorder.
XX Specifically, it refers to identifying modulators of two genes expressed
XX in the central nervous system of patients suffering from bipolar disorder
XX or schizophrenia, namely alpha-type II calcium/calmodulin dependent
XX protein kinase (CAMKII-alpha) and TBR1 (a putative transcription factor
XX related to the Brachyury gene). The present invention describes screening
XX assays used to identify gene expression modulators, as well as
XX appropriate antibodies, agonists and antagonists thereof. Accordingly,
XX these compositions, which exhibit neuroleptic and antidepressant
XX activities can also be used for gene therapy purposes to treat the
XX aforementioned conditions, and mental disorders including mood disorders,
XX psychosis and major depression. This polypeptide sequence is the human
XX CAMKI protein of the invention.
XX
XX SQ Sequence 370 AA;
```

## Alignment Scores:

|                        |         |               |     |
|------------------------|---------|---------------|-----|
| Pred. No.:             | 1.7e-89 | Length:       | 370 |
| Score:                 | 1184.50 | Matches:      | 220 |
| Percent Similarity:    | 85.53%  | Conservative: | 52  |
| Best Local Similarity: | 69.18%  | Mismatches:   | 43  |
| Query Match:           | 41.24%  | Indels:       | 3   |
| DB:                    | 8       | Gaps:         | 2   |

US-10-032-254A-1 (1-1554) x ADL97820 (1-370)

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Qy 120 AAACAGAGGAGGACATCAGCAGTGTCTATGATCGGAGAGCTGGGCTCGGTGCC 179
Db 11 LysGlnAlaGluAspIleArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla 30
Qy 180 TTCTCTGAGGTGATGCTGGCCAGGAAGGGCTCTGCTCATCTTGTGGCCCTCAAGTGC 239
Db 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50
Qy 240 ATTCCCAAGAAACACTTCGGGCGAAGGAGCCCTGGTGGAGATGAGATCGGGTACTT 299
Db 51 IleAlaLysGluAlaLeuGluGlyLysGluGlySerMetGluAsnGluIleAlaValLeu 70
Qy 300 CGCAGATCAGCCATCCCACTTGGCTCTGAGGAGCTCCATGAGATCTCTCAT 359
Db 71 HisLysIleLysHisProAsnIleValAlaLeuAspIleTyrGluSerGlyGlyHis 90
Qy 360 CTCTACTTGGCCATGGAGCTGTAACAGAGTGGTGAACACTGTTTGGACCCGATCATGGAGCGG 419
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Db 91 LeuTyrLeuLeuMetGlnLeuValSerGlyGlyLeuPheAspArgIleValGluLys 110
Qy 420 GGCTCTTACACAGAGAGGACCGCCAGCCACCTTGTAGGCGAGGTCTTGGCGTGTCTCC 479
Db 111 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130
Qy 480 TACCTTCATAGCCCTGGGATCGTGACCGGACCTCAAGCTGAAAACCTCTCTATGCC 539
Db 131 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuLeuTyr 150
Qy 540 ACACCTTTTGGAGCTCCAGATCATGCTCTGACTTTGGCTGTCCAAATACAA--- 596
Db 151 SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp 170
Qy 597 GCTGGCAACATCTAGGACACAGCTGTGGGACCCAGCATATGGCCCGCCAGAGCTCCTG 656
Db 171 ProGlySerValLeuSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeu 190
Qy 657 GAGCAGAAACCTACGGAAGCGGTAGATGTGTGGCCCTGGGTGTCTCTCTACATC 716
Db 191 AlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyrIle 210
Qy 717 CTGCTGTGTGGTACCCCTCTCTATGATGAGAGCGATCCTGAACTTTCAGCCAGATT 776
Db 211 LeuLeuCysGlyTyrProProPheTyrAspGluAsnAspAlaLysLeuPheGluGlnIle 230
Qy 777 CTGAGGCGAGCTATGATGTTGACTCCCTCTTGGGATGACATCTCAGAAATCAGCCAAA 836
Db 231 LeuLysAlaGluTyrGluPheAspSerProTyrTrpAspAlaLysSerAspSerAlaLys 250
Qy 837 GACTTCATCCGACCTTCTGGAACGTGATCCCCAGAGAGTTTCACTCCGACGAGGCC 896
Db 251 AspPheIleArgHisLeuMetGluLysAspProGluLysArgPheThrCysGluGlnAla 270
Qy 897 CTACAGCATCTTGGATCTCTGGGATGACGCTTCGATAGGAGACATCTCTGGTCTGTC 956
Db 271 LeuGlnHisProTyrIleAlaGlyAspThrAlaLeuAspLysAsnIleHisGlnSerVal 290
Qy 957 AGTGAGCAGATCCAGAGAATTTTCCAGGACCCACTGGAAGCGTGCATTCAATGCCACA 1016
Db 291 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 310
Qy 1017 TCATTCTACGTACATCCCTTAAG-----CTGGACAAAGCCAGAGGCTGAG 1064
Db 311 AlaValValArgHisMetArgLysLeuGlnLeuGlyThrSerGlnGluGlyGln 328
RESULT 15
ADP23704
XX ADP23704 standard; protein; 370 AA.
XX AC ADP23704;
XX DT 18-NOV-2004 (first entry)
XX DE PRO polypeptide SEQ ID NO:882.
XX KW PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
XX KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
XX KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
XX OS Unidentified.
XX PN W02004041170-A2.
XX PD 21-MAY-2004.
XX PF 30-OCT-2003; 2003WO-US034312.
XX PR 01-NOV-2002; 2002US-0423394P.
XX PA (GETH ) GENENTECH INC.
XX
```

```
PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
XX Wu TD;
DR WPI; 2004-419628/39.
XX N-PSDB; ADP23703.
PT New PRO polypeptides and polynucleotides, useful for treating e.g.
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT renal disease, or demyelinating diseases of the central or peripheral
PT nervous system.
XX Claim 7; SEQ ID NO 882; 2940pp; English.
PS The invention relates to a novel isolated nucleic acid and the PRO
CC polypeptide encoded by it. A protein of the invention has
CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
CC of the invention may have a use in gene therapy. The PRO polypeptide, its
CC agonist, antagonist, or antibody that specifically binds to the
CC polypeptide is useful for treating an immune related disorder such as
CC systemic lupus erythematous, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, a demyelinating disease of the central or peripheral nervous
CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplantation associated disease, graft rejection or
CC graft-versus-host disease. The present sequence represents a PRO protein
CC of the invention.
XX SQ Sequence 370 AA;
```

## Alignment Scores:

|                        |         |               |     |
|------------------------|---------|---------------|-----|
| Pred. No.:             | 1-7e-89 | Length:       | 370 |
| Score:                 | 1184.50 | Matches:      | 220 |
| Percent Similarity:    | 85.53%  | Conservative: | 52  |
| Best Local Similarity: | 69.18%  | Mismatches:   | 43  |
| Query Match:           | 41.24%  | Indels:       | 3   |
| DB:                    | 8       | Gaps:         | 2   |

US-10-032-254A-1 (1-1554) x ADP23704 (1-370)

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Db 11 LysGlnAlaGluAspIleArgAspIleTyrAspPheArgValLeuGlyThrGlyAla 30
Qy 180 TTCTCTGAGTGATGCTGGCCAGGAAAGGGCTCTGCTCATCTTGTGGCCCTCAAGTCC 239
Db 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50
Qy 240 ATTCCCAAGAAAGCACTTCGGGGCAGAGGCCCTGGTGAGAGATGAGTCGCGGTACTT 299
Db 51 IleAlaLysGluAlaLeuGluGlyLysGluGlySerMetGluAsnGluIleAlaValLeu 70
Qy 300 CGCAGAAATCAGCCATCCCAACATTTGGTCTCTGGAGACGCTCCATGAGAGTCTTCTCAT 359
Db 71 HisLysIleLysHisProAsnIleValAlaLeuAspAspIleTyrGluSerGlyGlyHis 90
Qy 360 CTCTACTTGGCCATGAGCTGGTAAACAGGTGGTGAACCTTTTGCACCCCATCATGGACGG 419
Db 91 LeuTyrLeuIleMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGluLys 110
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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 6, 2005, 09:50:10 ; Search time 45 Seconds  
(without alignments)

5155.762 Million cell updates/sec

Title: US-10-032-254A-1

Perfect score: 2872

Sequence: 1 gttcgaggatccctccactc.....caaaaaaaaaaaaaaaaaa 1554

Scoring table:

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Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Issued\_PatentsAA -QFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0

-LIST=0 -UNITS=bits -START=1 -END=1 -MATRIX=BLOSUM62 -TRANS=human40.cdi /

-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -ALIGN=15

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pep.\*

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6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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| 1          | 1808   | 63.0        | 358    | 4     | US-09-230-896C-29  |
| 2          | 1625   | 56.6        | 343    | 2     | US-08-878-989-5    |
| 3          | 1625   | 56.6        | 343    | 3     | US-09-272-796-5    |
| 4          | 1190   | 41.4        | 415    | 4     | US-09-949-016-7461 |
| 5          | 1190   | 41.4        | 415    | 4     | US-09-949-016-7462 |
| 6          | 1184.5 | 41.2        | 370    | 2     | US-08-878-989-19   |
| 7          | 1184.5 | 41.2        | 370    | 3     | US-09-272-796-19   |
| 8          | 1184.5 | 41.2        | 370    | 3     | US-09-457-0408-31  |
| 9          | 1184.5 | 41.2        | 370    | 4     | US-09-538-092-1314 |
| 10         | 1173.5 | 40.9        | 385    | 4     | US-09-733-388-2    |
| 11         | 1173.5 | 40.9        | 385    | 4     | US-10-446-175-2    |
| 12         | 1169.5 | 40.7        | 355    | 4     | US-09-579-664B-10  |

|    |        |      |     |   |                    |                   |
|----|--------|------|-----|---|--------------------|-------------------|
| 13 | 1169.5 | 40.7 | 355 | 4 | US-10-355-975A-10  | Sequence 10, Appl |
| 14 | 1157   | 40.3 | 356 | 4 | US-09-733-388-4    | Sequence 4, Appl  |
| 15 | 1157   | 40.3 | 356 | 4 | US-10-446-175-4    | Sequence 4, Appl  |
| 16 | 1065   | 37.1 | 476 | 4 | US-09-960-643-2    | Sequence 2, Appl  |
| 17 | 730    | 25.4 | 473 | 4 | US-09-538-092-1353 | Sequence 1353, Ap |
| 18 | 725    | 25.2 | 501 | 4 | US-09-734-030-2    | Sequence 2, Appl  |
| 19 | 725    | 25.2 | 501 | 4 | US-10-153-321-2    | Sequence 2, Appl  |
| 20 | 725    | 25.2 | 501 | 4 | US-09-797-039-2    | Sequence 2, Appl  |
| 21 | 725    | 25.2 | 501 | 4 | US-10-669-689-2    | Sequence 2, Appl  |
| 22 | 669    | 23.3 | 424 | 2 | US-08-715-568A-1   | Sequence 1, Appl  |
| 23 | 659    | 22.9 | 729 | 4 | US-09-949-016-6544 | Sequence 6544, Ap |
| 24 | 659    | 22.9 | 794 | 4 | US-09-949-016-9883 | Sequence 9883, Ap |
| 25 | 639.5  | 22.3 | 264 | 2 | US-07-857-326B-24  | Sequence 24, Appl |
| 26 | 637    | 22.2 | 766 | 4 | US-09-975-326-2    | Sequence 2, Appl  |
| 27 | 637    | 22.2 | 766 | 4 | US-10-217-357-2    | Sequence 2, Appl  |
| 28 | 634.5  | 22.1 | 765 | 4 | US-09-975-326-4    | Sequence 4, Appl  |
| 29 | 634.5  | 22.1 | 765 | 4 | US-10-217-357-4    | Sequence 4, Appl  |
| 30 | 594.5  | 20.7 | 264 | 2 | US-07-857-224B-18  | Sequence 18, Appl |
| 31 | 591    | 20.6 | 463 | 1 | US-07-951-715A-25  | Sequence 25, Appl |
| 32 | 591    | 20.6 | 463 | 2 | US-08-459-448A-25  | Sequence 25, Appl |
| 33 | 591    | 20.6 | 463 | 3 | US-08-459-595A-25  | Sequence 25, Appl |
| 34 | 591    | 20.6 | 463 | 3 | US-08-459-504B-25  | Sequence 25, Appl |
| 35 | 591    | 20.6 | 463 | 3 | US-08-459-444-25   | Sequence 0, Appl  |
| 36 | 591    | 20.6 | 463 | 3 | US-09-547-422-25   | Sequence 0, Appl  |
| 37 | 591    | 20.6 | 463 | 4 | US-09-988-462-25   | Sequence 25, Appl |
| 38 | 589.5  | 20.5 | 817 | 4 | US-09-992-481-4    | Sequence 4, Appl  |
| 39 | 589.5  | 20.5 | 817 | 4 | US-10-434-034-4    | Sequence 4, Appl  |
| 40 | 589    | 20.5 | 565 | 3 | US-09-800-960-2    | Sequence 2, Appl  |
| 41 | 589    | 20.5 | 565 | 4 | US-10-096-960-2    | Sequence 2, Appl  |
| 42 | 584.5  | 20.4 | 639 | 3 | US-09-347-801-17   | Sequence 17, Appl |
| 43 | 584.5  | 20.4 | 639 | 4 | US-09-854-731-17   | Sequence 17, Appl |
| 44 | 584    | 20.3 | 556 | 3 | US-09-800-960-4    | Sequence 4, Appl  |
| 45 | 584    | 20.3 | 556 | 4 | US-10-096-960-4    | Sequence 4, Appl  |

#### ALIGNMENTS

##### RESULT 1

US-09-230-896C-29  
; Sequence 29, Application US/09230896C  
; Patent No. 6635479

; GENERAL INFORMATION:  
; APPLICANT: The Scripps Research Institute  
; TITLE OF INVENTION: Hypothalamus-Specific Polypeptides  
; FILE REFERENCE: TSRI-548.1  
; CURRENT APPLICATION NUMBER: US/09/230,896C  
; CURRENT FILING DATE: 1999-02-02  
; PRIOR APPLICATION NUMBER: 60/023,220  
; PRIOR FILING DATE: 1996-08-02  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 358  
; TYPE: PRT  
; ORGANISM: ratus ratus  
US-09-230-896C-29

Alignment Scores:  
Pred. No.: 5.55e-158 Length: 358  
Score: 1808.00 Matches: 353  
Percent Similarity: 98.60% Conservative: 0  
Best Local Similarity: 98.60% Mismatches: 5  
Query Match: 62.95% Indels: 1  
DB: 4 Gaps: 0

US-10-032-254A-1 (1-1554) x US-09-230-896C-29 (1-358)

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Dy 1 MetLeuLeuLeuLysGlnThrGluAspSerValIyrGluIleArgGluLys 20  
Qy 165 CTGGGCTCGGGTGCCTTCTCTGAGGTGATGCTGCCCGGAAAGGGGCTCTGCTCATCTT 224

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Db 21 LeuGlySerGlyAlaPheSerGluValMetLeuAlaGlnGluArgGlySerAlaHisLeu 40
Qy 225 GTGGCCCTCAAGTCATTCCCAAGAACACACTTCGGGGCAAGAGGCCCTCGTGGAGAAAT 284
Db 41 ValAlaLeuLysCysIleProLysLeuAlaLeuArgGlyLysGluAlaLeuValGluAsn 60
Qy 285 GAGATCCGGTACTTCCGAGAAATCAGCCATCCCAACATTGTGGCTCTGGAGAGCGTCCAT 344
Db 61 GluIleAlaValLeuArgGlySerHisProAsnIleValAlaLeuGluAspValHis 80
Qy 345 GAGAGTCCTCTCATCTCTACTTGGCCATCGAGCTGTAACAGTGTGTGAAGTGTGTGAC 404
Db 81 GluSerProSerHisLeuTyrLeuAlaMetGluLeuValThrGlyGlyGluLeuPheAsp 100
Qy 405 CGCATCATGAGCGGGCTCTCTACACAGAGAAGACGCCAGCCACTTGTAGGCGCAGGTC 464
Db 101 ArgIleMetGluArgGlySerTyrThrGluLysAspAlaSerHisLeuValGlyGlnVal 120
Qy 465 CTGGCGCTGTCTCTACCTTATAGCTTGGGCTGTCGACCGGACCTCAAGCCTGAA 524
Db 121 LeuGlyAlaValSerTyrLeuHisSerLeuGlyIleValHisArgAspLeuLysProGlu 140
Qy 525 AACTCTCTATGTCACACCTTTTGGAGCTCCAAAGATCATGTCTCTGACTTTGGCCTG 584
Db 141 AsnLeuLeuTyrAlaThrProPheGluAspSerLysIleMetValSerAspPheGlyLeu 160
Qy 585 TCAAAAATACAAGCTGGCAACATCTAGGCACACCTGTGGGACCCAGGATATGTGGCC 644
Db 161 SerLysIleGlnAlaGlyAsnMetLeuGlyThrAlaCysGlyThrProGlyTyrValAla 180
Qy 645 CCAGAGCTCTGGAGCAGAAACCTTACGGGAAGCCCTAGATGTGGGCGCTGGGTGTC 704
Db 181 ProGluLeuLeuGluGlnLysProTyrGlyLysAlaValaAspValTProAlaLeuGlyVal 200
Qy 705 ATCTCTACATCTCTGCTGTGGGTACCCCTCTCTATGATGAGCGGATCTCTGAATC 764
Db 201 IleSerTyrIleLeuLeuCysGlyTyrProPheTyrAspGluSerAspProGluLeu 220
Qy 765 TTACAGCCAGATTTCTGAGGCGCAGCTATGAGTTTGCATCTCCCTTTTGGGATGACATCTCA 824
Db 221 PheSerGlnIleLeuArgAlaSerTyrGluPheAspSerProPheTyrAspAspIleSer 240
Qy 825 GAATCAGCCAAAGACTTCAATTCGCCACCTTCTGGAACGTGATCCCAAGAGAGTTTCAAC 884
Db 241 GluSerAlaLysAspPheIleArgHisLeuLeuGluArgAspProGlnLysArgPheThr 260
Qy 885 TGCCAGCAGGCCCTACAGCATCTTTGGATCTCTGGGATGCAGCTTCGATAGGCACATC 944
Db 261 CysGlnGlnAlaLeuGlnHisLeuTrpIleSerGlyAspAlaAlaLeuAspArgAspIle 280
Qy 945 CTGGGTTCCTGTAGTGAGCAGATCCAGAAGAAATTTGCCAGGACCCACTGGAAGCGTGCA 1004
Db 281 LeuGlySerValSerGluGlnIleGlnLysAsnPheAlaArgThrHisTyrLysArgAla 300
Qy 1005 TTCATGCCACATCTCTACGTCATCTGTAAGCTGGGACAAAGCCAGAGGGTGTAG 1064
Db 301 PheAsnAlaThrSerPheLeuArgHisIleArgLysLeuGlyGlnSerProGluGlyGlu 320
Qy 1065 GAGGCGCTCCAGGAGTGTATGACCCGTCATAGCCACCCAGGCGCTTGGGACTAGCCAGTCC 1124
Db 321 GluAlaSerArgGlnGlyMetThrArgHisSerHisProGlyLeuGlyThrSerGlnSer 340
Qy 1125 CCCAAGTGGTG-AAAACCAGGTAGATCCCAAGGAAGGCCCAAGTGACTGACTCC 1177
Db 341 ProlysTrpValThrThrArgTrpMetProArgLysAlaLysTrpThrAspSer 358
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## RESULT 2

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US-08-878-989-5
; Sequence 5, Application US/08878989
; Patent No. 5885803
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
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; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Survi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/878,989
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 343 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PROSNOT06
; CLONE: 827431
; US-08-878-989-5
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Alignment Scores:
Pred. No.: 4,05e-141 Length: 343
Score: 1625.00 Matches: 316
Percent Similarity: 93.29% Conservative: 4
Best Local Similarity: 92.13% Mismatches: 23
Query Match: 56.58% Indels: 0
DB: 2 Gaps: 0
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US-10-032-254A-1 (1-1554) x US-08-878-989-5 (1-343)

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Qy 105 ATGCTGTGCTCAAGAAACAGACGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAG 164
Db 1 MetLeuLeuLeuLysLysHisThrGluAspIleSerSerValTyrGluIleArgGluArg 20
Qy 165 CTGGGCTCGGGTGCCTTCTCTGAGGTGATGCTGCCAGAAAGGGCTCTGCTCATCTT 224
Db 21 LeuGlySerGlyAlaPheSerGluValValLeuAlaGlnGluArgGlySerAlaHisLeu 40
Qy 225 GTGGCCCTCAAGTGCATTCCTCAAGAAAGCACTTCGGGGCAAGAGGCCCTGGTGGAGAAT 284
Db 41 ValAlaLeuLysCysIleProLysLysAlaLeuArgGlyLysGluAlaLeuValGluAsn 60
Qy 285 GAGATCCGGTACTTCCGAGAAATCAGCCATCCCAACATTGTGGCTCTGGAGAGCGTCCAT 344
Db 61 GluIleAlaValLeuArgGlySerHisProAsnIleValAlaLeuGluAspValHis 80
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QY 345 GAGAGTCTCTCTCATCTCTACTTGGCCATGAGCTGTAAACAGGTGGTGAACCTTTTGAC 404
Db 81 GluSerProSerHisLeuTyrLeuAlaMetGluLeuValThrGlyGlyGluLeuPheAsp 100
QY 405 CGCATCATGAGCGGGCTCTACACAGAGAAGAGCCAGCCACCTTGAGGCGAGGTC 464
Db 101 ArgIleMetGluArgGlySerTyrThrGlyLeuAspAlaSerHisLeuValGlyGlnVal 120
QY 465 CTGCGGCTCTCTCTACCTTCTATAGCTCGTGGCATCGTCACCGGGACCTCAAGCCCTGAA 524
Db 121 LeuGlyAlaValSerTyrLeuHisSerLeuGlyLeuValHisArgAspLeuLysProGlu 140
QY 525 AACCTCTCTATGCCACACCTTTTGGAGACTCCAAGATCATGTCTCTGACTTTGGCCTG 584
Db 141 AsnLeuLeuTyrAlaThrProPheGluAspSerLysIleMetValSerAspPheGlyLeu 160
QY 585 TCCAAATACAACTGCAACCTGAGGACAGCCCTGTGGGACCCAGGATATGTGGCC 644
Db 161 SerLysIleGlnAlaGlyAsnMetLeuGlyThrAlaCysGlyThrProGlyTyrValAla 180
QY 645 CCAGAGCTCTCGAGCAGAAACCTTACGGGAAGCCGTAGATGTGTGGCCCTGGGTGTC 704
Db 181 ProGluLeuLeuGluGlnLysProTyrGlyLeuAlaValAspValThrAlaLeuGlyVal 200
QY 705 ATCTCTACATCTCTGTGTGTGGTACCCCTCTTCTATGATGAGAGCATCTGAACTC 764
Db 201 IleSerTyrIleLeuLeuCysGlyTyrProPheTyrAspGluSerAspProGluLeu 220
QY 765 TTGAGCCAGATCTTGAGGCGCAGCTATGAGTTTGACTCCCTCTTGGGATGACATCTCA 824
Db 221 PheSerGlnIleLeuArgAlaSerTyrGluPheAsp***ProPheTyrAspPheSer 240
QY 825 GAATCAGCCAAAGACTTCATTGCGCACCTTCTGGAACGTGATCCCAAGAGAGGTTCCAC 884
Db 241 GluSerGlyLysAspPheIleArgHisLeuLeuGluArgAspLeuGlnLysArgPheThr 260
QY 885 TGCAGCAGCCCTTACAGCATCTTTGGATCTCTGGGATGACGCTTCGATAGGACATC 944
Db 261 CysGlnGlnAlaLeuArgAspLeuThrIlePheTyrAspThrGlyPheGlyArgAspIle 280
QY 945 CTGGTCTCTGAGTGAGCAGATCCAGAAATTTGCCAGGACCCACTGGAGCGTGCA 1004
Db 281 LeuGlyPheValSerGluGlnIleArgLysAsnPheAlaThrThrHisTyrLysArgAla 300
QY 1005 TTCAATGCCACATCATCTCTACGTCACATCCGTAAGCTGGGACAAAGCCAGAGGGTGAG 1064
Db 301 PheAsnAlaThrLeuPheLeuArgHisIleArgLysLeuGlyGlnIleProGluGlyGlu 320
QY 1065 GAGGCTTCCAGGCGAGTGTATGACCCGTCATAGCCACCCAGGCGCTTGGGACTAGCCAGTCC 1124
Db 321 GlyAlaSerGluGlnGlyMet***ArgHisSerHis***GlyLeuArgAlaGlyGlnPro 340
QY 1125 CCAAGTGG 1133
Db 341 ProLysTyr 343
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## RESULT 3

US-09-272-796-5

; Sequence 5, Application US/09272796

; Patent No. 6207148

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Corley, Neil C.

; APPLICANT: Guegler, Karl G.

; APPLICANT: Lal, Preeti

; APPLICANT: Goli, Surva K.

; APPLICANT: Shah, Purvi

; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN

; TITLE OF INVENTION: KINASES

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

```
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/272,796
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/878,989
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 343 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PROSNOT06
; CLONE: 827431
; US-09-272-796-5
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## Alignment Scores:

|                        |           |               |     |
|------------------------|-----------|---------------|-----|
| Pred. No.:             | 4.05e-141 | Length:       | 343 |
| Score:                 | 1625.00   | Matches:      | 316 |
| Percent Similarity:    | 93.29%    | Conservative: | 4   |
| Best Local Similarity: | 92.13%    | Mismatches:   | 23  |
| Query Match:           | 56.58%    | Indels:       | 0   |
| DB:                    | 3         | Gaps:         | 0   |

US-10-032-254A-1 (1-1554) x US-09-272-796-5 (1-343)

|    |     |  |     |
|----|-----|--|-----|
| QY | 105 | ATCTGCTGCTCAAGAAACAGACGAGGACATCAGCATGCTCTATGATCCGCGAGAAG     | 164 |
| Db | 1   | MetLeuLeuLysLysHisThrGluAspIleSerSerValTyrGluIleArgGluArg    | 20  |
| QY | 165 | CTGGGCTCGGGTCCCTTCTCTGAGGTGATGCTGCCCGAGAAAGGGGCTCTGCTCATCTT  | 224 |
| Db | 21  | LeuGlySerGlyAlaPheSerGluValValLeuAlaGlnGluArgGlySerAlaHisLeu | 40  |
| QY | 225 | GTGGCCCTCAAGTGCATTCCTCAAGAAAGCACTTCGGGGCAAGAGGCCCTGGTGAGAAAT | 284 |
| Db | 41  | ValAlaLeuLysCysIleProLysLysAlaLeuArgGlyLysGluAlaLeuValGluAsn | 60  |
| QY | 285 | GAGATCGCGTACTTCGCAGAAATCAGCCATCCCAACATTTGGCTCTGGAGGAGCTCAT   | 344 |
| Db | 61  | GluIleAlaValLeuArgArgIleSerHisProAsnIleValAlaLeuGluAspValHis | 80  |
| QY | 345 | GAGATGCTCTCTCATCTTCTACTTGGCCATGAGTGGTAACAGTGGTGAACCTTTTGAC   | 404 |
| Db | 81  | GluSerProSerHisLeuTyrLeuAlaMetGluLeuValThrGlyGlyGluLeuPheAsp | 100 |
| QY | 405 | CGCATCATGAGCGGGCTCTCTACAGAGAAGAGCCAGCCACCTTGTAGGCGAGGTC      | 464 |
| Db | 101 | ArgIleMetGluArgGlySerTyrThrGluLysAspAlaSerHisLeuValGlyGlnVal | 120 |
| QY | 465 | CTTGGGCGCTCTCTCTACCTTCTATGCTGGGATCTGTCACCGGGACCTCAAGCCCTGAA  | 524 |
| Db | 121 | LeuGlyAlaValSerTyrLeuHisSerLeuGlyIleValHisArgAspLeuLysProGlu | 140 |

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QY 525 AACCTCTCTATGCCACACCTTTTGGAGGACTCCAAAGATCATGCTCTGACTTTGGCGTG 584
Db 141 AsnLeuLeuTyrAlaThrProPheGluAspSerLysIleMetValSerAspPheGlyLeu 160
QY 585 TCCAAATACAACTGCAACATGCTAGGCACAGCCTGTGGGACCCAGGATATGGCC 644
Db 161 SerLysIleGlnAlaGlyAsnMetLeuGlyThrAlaCysGlyThrProGlyTyrValAla 180
QY 645 CCAGAGCTCTGGAGCAGAAACCTTACGGGAAGCCCTAGATGTGTGGGCCCTGGGTGTC 704
Db 181 ProGluLeuLeuGluGlnLysProTyrGlyLeuAlaValAspValTrpAlaLeuGlyVal 200
QY 705 ATCTCTACATCTCTGTGTGGGTACCCCTCTCTATGATGAGAGCGATCTGAACTC 764
Db 201 IleSerTyrIleLeuLeuCysGlyTyrProPheTyrAspGluSerAspProGluLeu 220
QY 765 TTCAGCCAGATCTGAGGCCAGCTATGAGTTTGACTCCCTTTTGGGATGACATCTCA 824
Db 221 PheSerGlnIleLeuArgAlaSerTyrGluPheAsp***ProPheTrpAspAspIleSer 240
QY 825 GAATCAGCCAAAGACTTCATTCGCCACCTCTCTGGAACGTGATCCCCAGAAAGAGGTTCA 884
Db 241 GluSerGlyLysAspPheIleArgHisLeuLeuGluArgAspLeuGlnLysArgPheThr 260
QY 885 TGCAGAGCCCTTACAGCATCTTTGGATCTCTGGGATGACGCTTTCGATAGGACATC 944
Db 261 CysGlnGlnAlaLeuArgAspLeuTrpIlePheTrpAspThrGlyPheGlyArgAspIle 280
QY 945 CTGGGTCTCTGAGTGCAGATCCAGAAATTTTCCAGGACCCACTCGAAGCGTGCA 1004
Db 281 LeuGlyPheValSerGluGlnIleArgLysAsnPheAlaTrpThrHisTrpLysArgAla 300
QY 1005 TTCAATGCCACATCATCTTACGTGCATCCGTAAGCTGGGACAAAGCCAGAGGGTGAG 1064
Db 301 PheAsnAlaThrLeuPheLeuArgHisIleArgLysLeuGlyGlnIleProGluGlyGlu 320
QY 1065 GAGCCCTCCAGGCACTGTATGACCCGTATAGCCACCCAGGCTTGGGACTAGCCAGTCC 1124
Db 321 GlyAlaSerGluGlnGlyMet***ArgHisSerHis***GlyLeuArgAlaGlyGlnPro 340
QY 1125 CCCAAGTGG 1133
Db 341 ProlysTrp 343

RESULT 4
US-09-949-016-7461
; Sequence 7461, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7461
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7461

Alignment Scores:
Pred. No.: 5,68e-101 Length: 415
Score: 1190.00 Matches: 227
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Percent Similarity: 78.49% Conservative: 54
Best Local Similarity: 63.41% Mismatches: 53
Query Match: 41.43% Indels: 24
DB: 4 Gaps: 4

US-10-032-254A-1 (1-1554) x US-09-949-016-7461 (1-415)

QY 15 CCACCTCCGAGGCGCCAGGGGCCAAGCAGCGATTAGGTGG-----CTGCGT 59
Db 32 ProArgArgGlyAlaLeuAlaValValGlyGlyGlnTrpAlaMetLeuGlyAlaValGlu 51
QY 60 GGTGACTGTGTGTCGACAGGTGGCTGCAAGCAGGCGTGCACATGCTGCTCAAG 119
Db 52 GlyProArgTrp-----55
QY 120 AAACAGACGAGGACATCAGCAGTGTCTATGAGATCCGGAGAGAGTGGGCTCGGTGCC 179
Db 56 LysGlnAlaGluAspIleArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla 75
QY 180 TTCTCTGAGGTGATGTCGCCAGGAAAGGGCTCTGCTCATCTTTGTGGCCTCAAGTGC 239
Db 76 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 95
QY 240 ATTCCCAAGAAAGCACTTCGGGCAAGGAGGCCCTGCTGGAGAAATCAGATCGCGTACTT 299
Db 96 IleAlaLysGluAlaLeuGluGlyLysGluGlySerMetGluAsnGluIleAlaValLeu 115
QY 300 CGCAGATCAGCCATCCCAACATTGTGGCTCTGGAGACGTCATCAGAGTCTCTTCAT 359
Db 116 HisLysIleLysHisProAsnIleValAlaLeuAspAspIleTyrGluSerGlyGlyHis 135
QY 360 CTCTACTTGGCCATGAGGTGTAAACAGGTGTGTAACCTTTTACCGCATCATGGACGG 419
Db 136 LeuTyrLeuIleMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGluLys 155
QY 420 GGCTCTCTACACAGAGAGGAGCCACCTTGTAGGCGAGCTCTTGGCGTGTCTCC 479
Db 156 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 175
QY 480 TACCTTCATAGCTCGGCATCTGTGCACCGGACCTCAAGCCTGAAACCTCTCTATGCC 539
Db 176 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuLeuTyr 195
QY 540 ACACCTTTTGAGGACTCCAAGATCATGTCTCTGACTTTGGCCTGTCCAAATAACAA--- 596
Db 196 SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp 215
QY 597 GCTGGCAACATGCTAGGCACAGCTGTGGGACCCAGGATATGTGGCCCGCAGAGCTCTG 656
Db 216 ProGlySerValLeuSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeu 235
QY 657 GAGCAGAAACCCCTACCGGAGGCGGTAGATGTGTGGGCCCTGGGTGTCTCTCTACATC 716
Db 236 AlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyrIle 255
QY 717 CTGCTGTGGGTACCCCGCTCTATGATGAGAGCGATCTGAACTCTTCAGCCACATT 776
Db 256 LeuLeuCysGlyTyrProPheTyrAspGluAsnAspAlaLysLeuPheGluGlnIle 275
QY 777 CTGAGGCGCAGCTATGAGTTTGATCTCCCTTTTGGGATGACATCTCAGAAATCAGCAAA 836
Db 276 LeuLysAlaGluTyrGluPheAspSerProTyrTrpAspAspIleSerAspSerAlaLys 295
QY 837 GACTTCATTCGCCACCTCTCTGGAACGTGATCCCCAGAAAGGTTTACCTCCAGCAGGCC 896
Db 296 AspPheIleArgHisLeuMetGluLysAspProGluLysArgPheThrCysGluGlnAla 315
QY 897 CTACAGCATCTTTGGATCTCTGGGATGAGCCCTTGATAGGACATCTCTGGGTCTGTC 956
Db 316 LeuGlnHisProTrpIleAlaGlyAspThrAlaLeuAspLysAsnIleHisGlnSerVal 335
QY 957 AGTGAGCAGATCCAGAAAGATTTTGGCAGGACCCACTGGGAAGCGTGCATTCAATGCCACA 1016
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Db 336 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 355  
Qy 1017 TCATTCTACGTACATCCCGTAAG-----CTGGGACAAAGCCAGAGGGTGAG 1064  
Db 356 AlaValValArgHisMetArgLysLeuGlnLeuGlyThrSerGlnGluGlyGln 373  
RESULT 5  
US-09-949-016-7462  
; Sequence 7462, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7462  
; LENGTH: 415  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-7462  
Alignment Scores:  
Pred. No.: 5.68e-101 Length: 415  
Score: 1190.00 Matches: 227  
Percent Similarity: 78.49% Conservative: 54  
Best Local Similarity: 63.41% Mismatches: 53  
Query Match: 41.43% Indels: 24  
DB: 4 Gaps: 4  
US-10-032-254A-1 (1-1554) x US-09-949-016-7462 (1-415)  
Qy 15 CCACTCCGAGCGCCAGCGGCCAGCAGCATGATAGTGG-----CTCGGT 59  
Db 32 ProArgArgGlyAlaLeuAlaValAlaValGlyGlyGlnTrpAlaMetLeuGlyAlaValGlu 51  
Qy 60 GGGTGACTGGTGGTGCACAGGTGGCTGCAAGCGGTCGACAGCATGCTGCTCAAG 119  
Db 52 GlyProArgTrp----- 55  
Qy 120 AAACAGACGGAGGACATCAGCAGTGTCTATGAGATCGGGAGAGCTGGGCTCGGGTGCC 179  
Db 56 LysGlnAlaGluAspIleArgAspIleTyAspPheArgAspValLeuGlyThrGlyAla 75  
Qy 180 TTCTCTGAGTGATGTCGGCCAGGAAAGGGCTCTGCTCATCTGTGGCCCTCAAGTC 239  
Db 76 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 95  
Qy 240 ATTCCCAAGAAAGCACTTCGGGCAAGAGCCCTGGTGAGATGAGATGAGTCGGGTACTT 299  
Db 96 IleAlaLysGluAlaLeuGluGlyLysGlySerMetGluAsnGluIleAlaValLeu 115  
Qy 300 CGCAGATCAGCCATCCCAATGTCCTCTGGAGAGCGTCATGAGATGCTTCTCAT 359  
Db 116 HisLysLysHisProAsnIleValAlaLeuAspAspIleTyGluSerGlyGlyHis 135  
Qy 360 CTCTACTGGCCATGGAGCTGGTAACAGGTGGTGAAGTCTGTGACCGCATCATGAGCGG 419  
Db 136 LeuTyrlLeuIleMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGluLys 155  
Qy 420 GGCTCTACAGAGAGAGCCAGCCAGTCCTGTAGGGCAGGTCCTTGGCGGTGCTCC 479  
Db 156 GlyPheTyThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 175

Qy 480 TACCTTCATAGCTGGGCATCGTGCACCGGACCTCAAGCCTGAAACCTCTCTATGCC 539  
Db 176 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuLeuTyTr 195  
Qy 540 ACACCTTTTTCAGGACTCCCAAGATCATGGTCTCTGACTTTTCGCTGTCACAAATACAA-- 596  
Db 196 SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp 215  
Qy 597 GCTGGCAACATGCTAGGCACAGCCTGTGGGACCCCGAGATATGTGGCCCGCAGAGCTCTG 656  
Db 216 ProGlySerValLeuSerThrAlaCysGlyThrProGlyTyValAlaProGluValLeu 235  
Qy 657 GACGACAAACCTACGGGAAGCGGTAGATGTGTGGCCCTGGGTGTCATCTCTCATATC 716  
Db 236 AlaGlnLysProTyTrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyTr 255  
Qy 717 CTGCTGTGTGGTACCCCTCTCTATGATGAGAGCGATCTGAACTTTTCAGCCAGATT 776  
Db 256 LeuLeuCysGlyTyTrProPheTyAspGluAsnAspAlaLysLeuPheGluGlnIle 275  
Qy 777 CTGAGGCGCAGCTATGATGTTGATCTCCCTTTTGGGATGACATCTCAGAAATCAGCCAAA 836  
Db 276 LeuLysAlaGluTyTrGluPheAspSerProTyTrPheAspIleSerAspSerAlaLys 295  
Qy 837 GACTTCATTCGCCACCTTCTGGAACGTGATCCCGAGAGAGGTTACCTGCCAGCAGGCC 896  
Db 296 AspPheIleArgHisLeuMetGluLysAspProGluLysArgPheThrCysGluGlnAla 315  
Qy 897 CTACAGCATCTTTGGATCTCTGGGGATGACCTTCGATAGGAGACATCTGGGTCTGTC 956  
Db 316 LeuGlnHisProTrpIleAlaGlyAspThrAlaLeuAspLysAsnIleHisGlnSerVal 335  
Qy 957 AGTGAGCAGATCCAGAAAGATTTTGGCAGCACCACCTGGGAAGCGTGCATTCATCAATGCCACA 1016  
Db 336 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 355  
Qy 1017 TCATTCTACGTACATCCCGTAAG-----CTGGGACAAAGCCAGAGGGTGAG 1064  
Db 356 AlaValValArgHisMetArgLysLeuGlnLeuGlyThrSerGlnGluGlyGln 373  
RESULT 6  
US-08-878-989-19  
; Sequence 19, Application US/08878989  
; Patent No. 5885803  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl G.  
; APPLICANT: Lal, Preeti  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN  
; TITLE OF INVENTION: KINASES  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/878,989  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:

```
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
;
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 370 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 790790
;
US-08-878-989-19
Alignment Scores:
Pred. No.: 1.72e-100 Length: 370
Score: 1184.50 Matches: 220
Percent Similarity: 85.53% Conservative: 52
Best Local Similarity: 69.18% Mismatches: 43
Query Match: 41.24% Indels: 3
DB: 2 Gaps: 2

US-10-032-254A-1 (1-1554) x US-08-878-989-19 (1-370)
QY 120 AAACAGAGGAGGACATCAGCATGCTCTATGAGATCCGGGAGAGCTGGGCTGGGTGCC 179
Db 11 LysGlnAlaGluAspIleArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla 30
QY 180 TTCTCTCAGGTGATCGTGGCCAGGAAAGGCTCTCTCATCTGTGGCCCTCAAGTGC 239
Db 31 PheSerGluValIleLeuAlaGluAspIleArgThrGlnLysLeuValAlaIleLysCys 50
QY 240 ATTCCTCCAGAAAGCACTTCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 299
Db 51 IleAlaLysGluAlaLeuGluGlyLysGluGlySerMetGluAsnGluIleAlaValLeu 70
QY 300 CGCAGATCAGCCATCCCAACATTTGCTGCTCTGAGGAGGAGGAGGAGGAGGAGGAGG 359
Db 71 HisLysIleLysHisProAsnIleValAlaLeuAspIleTyrGluSerGlyGlyHis 90
QY 360 CTCTACTTGGCCATGGAGTGTAAACAGGTGGTCAACTTTTACCGCATCATCGAGCGG 419
Db 91 LeuTyrLeuIleMetGlnLeuValIleSerGlyGlyLeuPheAspArgIleValGluLys 110
QY 420 GGCTCTTACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 479
Db 111 GlyPheTyrThrGluAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130
QY 480 TACCTTCATAGCTGGGATGTCACCGGACCTCAAGCTGAAACCTCTCTATGCC 539
Db 131 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuLeuTyr 150
QY 540 ACACCTTTTGGAGGACTCCAAAGATCATGTCTGACTTTTGGCTGTGCCAAATACAA- 596
Db 151 SerLeuAspGluAspSerLysIleLeuIleSerAspPheGlyLeuSerLysMetGluAsp 170
QY 597 GCTGGCAACCTTAGGACAGCCTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 656
Db 171 ProGlySerValLeuSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeu 190
QY 657 GAGCAGAAACCTTAGGAGAGCGGTAGATGTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 716
Db 191 AlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyrIle 210
QY 717 CTGTGTGTGGGTACCCCTCTCTATGATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 776
Db 211 LeuLeuCysGlyTyrProProPheTyrAspGluAsnAspAlaLysLeuPheGluGlnIle 230

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
;
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 370 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 790790
;
US-09-272-796-19
Alignment Scores:
Pred. No.: 1.72e-100 Length: 370
Score: 1184.50 Matches: 220
Percent Similarity: 85.53% Conservative: 52
Best Local Similarity: 69.18% Mismatches: 43
Query Match: 41.24% Indels: 3
DB: 2 Gaps: 2

US-09-272-796-19
QY 777 CTGAGGGCCAGCTATGAGTTGACTCCCTTTTGGGATGACATCTCAGATCAGCCAAA 836
Db 231 LeuLysAlaGluTyrGluPheAspSerProTyrTrpAspAspIleSerAspSerAlaLys 250
QY 837 GACTTCATTCCGCACCTCTCGAAAGCTGATCCCGCAGAGAGGTTACCTGCCAGCAGGCC 896
Db 251 AspPheIleArgHisLeuMetGluLysAspProGluLysArgPheThrCysGluGlnAla 270
QY 897 CTACAGCATCTTTGGATCTCTGGGAGTGCAGCTTCGATAGGAGACATCTGGGTTCTGTC 956
Db 271 LeuGlnHisProTyrPheAlaGlyAspThrAlaLeuAspLysAsnIleHisGlnSerVal 290
QY 957 AGTGAGCAGATCCAGAGAGATTTTGCAGAGCCCTGGAAGCGTGCATTCAATGCCACA 1016
Db 291 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 310
QY 1017 TCATTCTACGTACATCCGTAAAG-----CTGGGACAAAGCCCGCAGAGGAGTGGAG 1064
Db 311 AlaValValArgHisMetArgLysLeuGlnLeuGlyThrSerGlnGluGlyGln 328

RESULT 7
US-09-272-796-19
; Sequence 19, Application US/09272796
; Patent No. 6207148
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Survi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/272,796
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/878,989
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 370 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 790790
;
US-09-272-796-19
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Alignment Scores:
Pred. No.: 1.72e-100 Length: 370
Score: 1184.50 Matches: 220
Percent Similarity: 85.53% Conservative: 52
Best Local Similarity: 69.18% Mismatches: 43
Query Match: 41.24% Indels: 3
DB: 2
Gaps: 2

US-10-032-254A-1 (1-1554) x US-09-272-796-19 (1-370)

Qy 120 AACACAGCGAGGACATCAGCAGTGTCTATGAGATCCGGAGAGCTGGGCTCGGTGCC 179
Db 11 LysGlnAlaGluAspIleArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla 30
Qy 180 TTCTCTGAGGTGATGCTGGCCAGCAAGAGGGCTCTGCTCATCTTGTGGCCCTCAAGTGC 239
Db 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50
Qy 240 ATTCCCAAGAAGCACTTCGGGGCAAGAGGCCCTGTGGAGAAATGAGATCGCGGTACTT 299
Db 51 IleAlaLysGluAlaLeuGluGlyLysGluGlySerMetGluAsnGluIleAlaValLeu 70
Qy 300 CGCAGATCACCATCCCAACATTTGGCTCTGAGGACCTCATGAGTCTCTCTCAT 359
Db 71 HisLysIleLysHisProAsnIleValAlaLeuAspIleTyrGluSerGlyGlyHis 90
Qy 360 CTCTACTTTGGCCATGAGTGTAAACAGGTGGTAAACAGGTGGTAAACAGGTGGTAAAC 419
Db 91 LeuTyrLeuIleMetGlnLeuValSerGlyGlyLysLeuValSerGlyGlyLys 110
Qy 420 GGCTCTTACACAGAGAGGACCGCCACCTTCTAGGAGACGTCCTAGGAGGCTCTCTCC 479
Db 111 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130
Qy 480 TACTTCTATGCTGGGCATCTGTCACCGGACCTCAAGCTGAAACCTCTCTATGCC 539
Db 131 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuLeuTyr 150
Qy 540 ACACCTTTTGGAGACTCCAAAGATCATGCTCTGACTTTTGGCTGTCTCAAAATACAA 596
Db 151 SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp 170
Qy 597 GCTGGCAACATGCTAGCACAGCCTGTGGGACCCAGGATATGTGGGCTGTCTCTCC 656
Db 171 ProGlySerLeuSerThrAlaCysGlyThrProGlyThrValAlaProGluValLeu 190
Qy 657 GAGCAGAAACCTTACGAGAGCGGTAGATGTGTGGCCCTCTGGGTGTCTCTCTACATC 716
Db 191 AlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyrIle 210
Qy 717 CTGCTGTGTGGTACCCCTCTTATGATGAGAGCATCTGAACTTTCAGCCAGATT 776
Db 211 LeuLeuCysGlyTyrProPheTyrAspGluAsnAspAlaLysLeuPheGluGlnIle 230
Qy 777 CTGAGGCGCACTATGAGTTGATCCCTCTTGGGATGATCTCAGAAATCAGCAAA 836
Db 231 LeuLysAlaGluTyrGluPheAspSerProTyrTrpAspAspIleSerAspSerAlaLys 250
Qy 837 GACTTCAATCCCACTTCTGGAACGTGATCCCAAGAGGTTTCACTGTGCCAGCAGGCC 896
Db 251 AspPheIleArgHisLeuMetGluLysAspProGluLysArgPheThrCysGluGlnAla 270
Qy 897 CTACAGCATCTTTGGATCTCTGGGGATGACCCCTTCGATAGGACATCTCTGGGTCTGTC 956
Db 271 LeuGlnHisProTyrIleAlaGlyAspThrAlaLeuAspLysAsnIleHisGlnSerVal 290
Qy 957 AGTCAGCAGATCCAGAGAATTTTGGCAGGACCCACTGAGAGCGTGTCAATGACCCACA 1016
Db 291 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 310
Qy 1017 TCATTCTCTACATCCCGTAAG-----CTGGGCAAAAGCCCGAGGGGTGAG 1064
Db 1017 TCATTCTCTACATCCCGTAAG-----CTGGGCAAAAGCCCGAGGGGTGAG 1064
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Db 311 AlaValValArgHisMetArgLysLeuGlnLeuGlyThrSerGlnGluGlyGln 328

RESULT 8  
US-09-457-040B-31  
; Sequence 31 Application US/09457040B  
; Patent No. 6387641  
; GENERAL INFORMATION:  
; APPLICANT: Vertex Pharmaceuticals Incorporated  
; TITLE OF INVENTION: Crystallized P38 Complexes  
; FILE REFERENCE: VPI/98-14  
; CURRENT APPLICATION NUMBER: US/09/457,040B  
; CURRENT FILING DATE: 1999-12-08  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 31  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Human  
; US-09-457-040B-31

Alignment Scores:  
Pred. No.: 1.72e-100 Length: 370  
Score: 1184.50 Matches: 220  
Percent Similarity: 85.53% Conservative: 52  
Best Local Similarity: 69.18% Mismatches: 43  
Query Match: 41.24% Indels: 3  
DB: 2  
Gaps: 2

US-10-032-254A-1 (1-1554) x US-09-457-040B-31 (1-370)

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Qy 120 AACACAGCGAGGACATCAGCAGTGTCTATGAGATCCGGAGAGCTGGGCTCGGTGCC 179
Db 11 LysGlnAlaGluAspIleArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla 30
Qy 180 TTCTCTGAGGTGATGCTGGCCAGCAAGAGGGCTCTGCTCATCTTGTGGCCCTCAAGTGC 239
Db 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50
Qy 240 ATTCCCAAGAAGCACTTCGGGGCAAGAGGCCCTGTGGAGAAATGAGATCGCGGTACTT 299
Db 51 IleAlaLysGluAlaLeuGluGlyLysGluGlySerMetGluAsnGluIleAlaValLeu 70
Qy 300 CGCAGATCACCATCCCAACATTTGGCTCTGAGGACGTCCTAGGAGGCTCTCTCAT 359
Db 71 HisLysIleLysHisProAsnIleValAlaLeuAspIleTyrGluSerGlyGlyHis 90
Qy 360 CTCTACTTTGGCCATGAGTGTAAACAGGTGGTAAACAGGTGGTAAACAGGTGGTAAAC 419
Db 91 LeuTyrLeuIleMetGlnLeuValSerGlyGlyLysLeuValSerGlyGlyLys 110
Qy 420 GGCTCTTACACAGAGAGGACCGCCACCTTCTAGGAGACGTCCTAGGAGGCTCTCTCC 479
Db 111 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130
Qy 480 TACTTCTATGCTGGGCATCTGTCACCGGACCTCAAGCTGAAACCTCTCTATGCC 539
Db 131 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuLeuTyr 150
Qy 540 ACACCTTTTGGAGACTCCAAAGATCATGCTCTGACTTTTGGCTGTCTCAAAATACAA 596
Db 151 SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp 170
Qy 597 GCTGGCAACATGCTAGCACAGCCTGTGGGACCCAGGATATGTGGGCTGTCTCTCC 656
Db 171 ProGlySerLeuSerThrAlaCysGlyThrProGlyThrValAlaProGluValLeu 190
Qy 657 GAGCAGAAACCTTACGAGAGCGGTAGATGTGTGGCCCTCTGGGTGTCTCTCTACATC 716
Db 191 AlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyrIle 210
Qy 717 CTGCTGTGTGGTACCCCTCTTATGATGAGAGCATCTGAACTTTCAGCCAGATT 776
Db 211 LeuLeuCysGlyTyrProPheTyrAspGluAsnAspAlaLysLeuPheGluGlnIle 230
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-733-388-2

Alignment Scores:
Pred. No.: 1.82e-99 Length: 385
Score: 1173.50 Matches: 216
Percent Similarity: 85.09% Conservative: 58
Best Local Similarity: 67.08% Mismatches: 45
Query Match: 40.86% Indels: 3
DB: 4 Gaps: 2

US-10-032-254A-1 (1-1554) x US-09-733-388-2 (1-385)
Qy 117 AAGAAACAGACGAGGACATCAGCAGTCTCTATGAGATCCGGGAGAGCTGGGCTCGGT 176
Db 13 LysLysGlnAlaGluAspIleLysAlaPheGluPheLysGluThrLeuGlyThrGly 32
Qy 177 GCCTTCTCTGAGTGATGCTGGCCCAAGAAAGGGCTCTGCTCATCTTTGGCCCTCAAG 236
Db 33 AlaPheSerGluValValLeuAlaGluLysAlaThrGlyLysLeuPheAlaVallys 52
Qy 237 TGCATTCCCAAGAACACATTCGGGGCAAGAGGCCCTCTGGAGAGATGATCGCGTA 296
Db 53 CysIleProLysLysAlaLeuLysGlyLysSerSerIleGluAenGluAlaVal 72
Qy 297 CTTTCGAGATACGCCATCCCAACATTTGGCTCTGGAGACGTCATGAGTCTTCT 356
Db 73 LeuArgLysIleLysHisGluAenIleValAlaLeuGluAspIleTyrGluSerProAsn 92
Qy 357 CATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTAACCTTTGACCGCATCGGAG 416
Db 93 HisLeuTyrLeuValMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGlu 112
Qy 417 CGGGGCTCTTACACAGAGAGGACGCCAGCCACTTGTAGGGAGGTCCTTGGCGCTGC 476
Db 113 LysGlyPheTyrThrGluLysAspAlaSerThrLeuIleArgGlnValLeuAspAlaVal 132
Qy 477 TCCTACCTTCATAGCCTGGGCATCGTGCACGGGACCTCAAGCCTGAAACCTCTCTAT 536
Db 133 TyrTyrLeuHisArgMetGlyIleValHisArgAspLeuLysProGluAenLeuLeuTyr 152
Qy 537 GCCACACTTTTGGAGGATCCAAGATCATGCTCTGACTTTGGCTGTGCTCCAAATAACA 596
Db 153 TyrSerGlnAspGluGluSerLysIleMetIleSerAspPheGlyLeuSerLysMetGlu 172
Qy 597 GCT---GGCAACATGCTAGGACAGCCTGTGGAGCCCAAGATATGTGGCCCGCAGCTC 653
Db 173 GlyLysGlyAspValMetSerThrAlaCysGlyThrProGlyTyrValAlaProGluVal 192
Qy 654 CTGGAGCAGAAACCTACGGGAGCGGTAGATGTGTGGCCCTGGGTGTCATCTCCTAC 713
Db 193 LeuAlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyr 212
Qy 714 ATCCTGTGTGTGGGTACCCCTCTCTATGATGAGAGCATCTCTGAACCTTTCAGCCAG 773
Db 213 IleLeuLeuCysGlyTyrProProPheTyrAspGluAsnAspSerLysLeuPheGluGln 232
Qy 774 ATTCTGAGGCGAGCTATGAGTTGACTCCCTCTTGGGATGATCATCTCAGAAATCAGCC 833
Db 233 IleLeuLysAlaGluTyrGluPheAspSerProTyrTrpAspAspIleSerAspAla 252
Qy 834 AAGACTTTCAGCCACTCTGGAACGTGATCCCGAGAGAGGTTCCACTCGCCAGCAG 893
Db 253 LysAspPheIleArgAenLeuMetGluLysAspProAenLysArgTyrThrCysGluGln 272
Qy 894 GCCCTACAGCATCTTTGGATCTCTGGGGATGCAGCCCTTCAGATAGGACATCTCGGTCT 953
Db 273 AlaAlaArgHisProTyrPleAlaGlyAspThrAlaLeuAenLysAenIleHisGluSer 292
Qy 954 GTCAGTGAGGAGATCCAGAGAAATTTTCCAGGACCCACTGGAGCGCTGATTCATTCGCC 1013
Db 293 ValSerAlaGlnIleArgLysAenPheAlaLysSerLysTrpArgGlnAlaPheAsnAla 312
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Qy 1014 ACATCATTTCTACGTCACATCCGTAAG-----CTGGGACAAAGCCACAGAGGTGAGGAG 1067
Db 313 ThrAlaValValArgHisMetArgLysLeuHisLeuGlySerSerLeuAspSerSerAsn 332

Qy 1068 GCCTCC 1073
Db 333 Alaser 334

RESULT 11
US-10-446-175-2
; Sequence 2, Application US/10446175
; Patent No. 6806073
; GENERAL INFORMATION:
; APPLICANT: Donoho, Greg
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Abuin, Alejandro
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6806073el Human Kinase Proteins and
; FILE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0103-USA
; CURRENT APPLICATION NUMBER: US/10/446,175
; PRIOR FILING DATE: 2003-05-27
; PRIOR APPLICATION NUMBER: US/09/733,388
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,428
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-446-175-2

Alignment Scores:
Pred. No.: 1.82e-99 Length: 385
Score: 1173.50 Matches: 216
Percent Similarity: 85.09% Conservative: 58
Best Local Similarity: 67.08% Mismatches: 45
Query Match: 40.86% Indels: 3
DB: 4 Gaps: 2

US-10-032-254A-1 (1-1554) x US-10-446-175-2 (1-385)
Qy 117 AAGAAACAGACGAGGACATCAGCAGTCTCTATGAGATCCGGGAGAGCTGGGCTCGGT 176
Db 13 LysLysGlnAlaGluAspIleLysAlaPheGluPheLysGluThrLeuGlyThrGly 32
Qy 177 GCCTTCTCTGAGTGATGCTGGCCCAAGAAAGGGCTCTGCTCATCTTTGGCCCTCAAG 236
Db 33 AlaPheSerGluValValLeuAlaGluLysAlaThrGlyLysLeuPheAlaVallys 52
Qy 237 TGCATTCCCAAGAACACATTCGGGGCAAGAGGCCCTCTGGAGAGATGATCGCGTA 296
Db 53 CysIleProLysLysAlaLeuLysGlyLysSerSerIleGluAenGluAlaVal 72
Qy 297 CTTTCGAGATACGCCATCCCAACATTTGGCTCTGGAGACGTCATGAGTCTTCT 356
Db 73 LeuArgLysIleLysHisGluAenIleValAlaLeuGluAspIleTyrGluSerProAsn 92
Qy 357 CATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTAACCTTTGACCGCATCGGAG 416
Db 93 HisLeuTyrLeuValMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGlu 112
Qy 417 CGGGGCTCTTACACAGAGAGGACGCCAGCCACTTGTAGGGAGGTCCTTGGCGCTGC 476
Db 113 LysGlyPheTyrThrGluLysAspAlaSerThrLeuIleArgGlnValLeuAspAlaVal 132
Qy 477 TCCTACCTTCATAGCCTGGGCATCGTGCACGGGACCTCAAGCCTGAAACCTCTCTAT 536
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|----|------|--|------|
| Db | 133  | TyTyrLeuHisArgMetGlyIleValHisArgAspLeuLysProGluAsnLeuLeuTyr    | 152  |
| Qy | 537  | GCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTGGCCCTGCCAAATACAA      | 596  |
| Db | 153  | TySerGlnAspGluGluSerLysIleMetIleSerAspPheGlyLeuSerLysMetGlu    | 172  |
| Qy | 597  | GCT---GGCAACATGCTAGGCACAGCTGTGGGACCCACAGGATATGGGCCCCAGAGCTC    | 653  |
| Db | 173  | GlyLysGlyAspValMetSerThrAlaCysGlyThrProGlyTyrValAlaProGluVal   | 192  |
| Qy | 654  | CTGGAGCAGAAACCTCATGGGAAGCCGTAGATCTGTGGGCCCTGGGTGTCACTCCTCAC    | 713  |
| Db | 193  | LeuAlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyr   | 212  |
| Qy | 714  | ATCTGTCTGTGTGGGTACCCCTTCTTATGATGAGAGCGATCTCTGAATCTTTCAGCCAG    | 773  |
| Db | 213  | IleLeuLeuCysGlyTyrProPheTyrAspGluAsnAspSerLysLeuPheGluGln      | 232  |
| Qy | 774  | ATTCTGAGGGCCACTATGAGTTTGACTCCCTCTTTGGGATGACATCTCAGAAATCAGCC    | 833  |
| Db | 233  | IleLeuLysAlaGluTyrGluPheAspSerProTyrTrpAspIleSerAspSerAla      | 252  |
| Qy | 834  | AAAGACTTCATTCGCCACCTTCTGGAACTGATCCCAGAAAGAGGTTCACTGCCACAGAG    | 893  |
| Db | 253  | LysAspPheIleArgAsnLeuMetGluLysAspProAsnLysArgTyrThrCysGluGln   | 272  |
| Qy | 894  | GCCCTACAGCATCTTGATCTCTGGGGATGCACGCTTCGATAGGACATCTCTGGGTCT      | 953  |
| Db | 273  | AlaAlaArgHisProTrpIleAlaGlyAspThrAlaLeuAsnLysAsnIleHisGluSer   | 292  |
| Qy | 954  | GTCACTGAGCAGATCCAGAAAGATTTTGGCCAGGACCCACTGGAAAGCGTGCAATCAATGCC | 1013 |
| Db | 293  | ValSerAlaGlnIleArgLysAsnPheAlaLysSerLysTrpArgGlnAlaPheAsnAla   | 312  |
| Qy | 1014 | ACATCATCTCTACGTCACTCCGTAAG-----CTGGGACAAAGCCACAGAGGGTGAGAG     | 1067 |
| Db | 313  | ThrAlaValValArgHisMetArgLysLeuHisLeuGlySerSerLeuAspSerSerAsn   | 332  |
| Qy | 1068 | GCCTCC   | 1073 |
| Db | 333  | AlaSer   | 334  |

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RESULT 12
US-09-579-664B-10
; Sequence 10, Application US/09579664B
; Patent No. 6514719
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
; FILE REFERENCE: 2923-A
; CURRENT APPLICATION NUMBER: US/09/579,664B
; CURRENT FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-579-664B-10

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US-10-032-254A-1 (1-1554) x US-09-579-664B-10 (1-355)

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| QY | 117  | AAAGAAACAGACGACGAGACATCAGCAGTGCTATGAGATCCGGAGAAAGCTGGGCTCGGGT  | 176  |
| Db | 13   | LysLysGlnAlaGluAspIleLysLysIlePheGluPheLysGluThrLeuGlyThrGly   | 32   |
| QY | 177  | GCCTTCTCTGAGGTGATGCTGGCCAGGAAGAGGGCTCTCTCATCTTTGTGGCCCTCAAG    | 236  |
| Db | 33   | AlaPheSerGluValLeuAlaGluGluAlaThrGlyLysLeuPheAlaValLys         | 52   |
| QY | 237  | TGCATTCCCAAGAAAGCACTTCGGGCCAAGGAGCCCTGCTGGAGATGAGATCGCGGTA     | 296  |
| Db | 53   | CysIleProLysLysAlaLeuLysGlyLysGluSerIleGluAsnGluIleAlaVal      | 72   |
| QY | 297  | CTTCGAGAATCAGCCATCCCAACTTGTGGCTCTGGAGGACGTCCATGAGAGTCCTTCT     | 356  |
| Db | 73   | LeuArgLysIleLysHisGluAsnIleValAlaLeuGluAspIleTyrGluSerProAsn   | 92   |
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| QY | 477  | TCCTTACCTTCATAGCTTGGCGATCTGTCACCGGGACCTCAAGCTGAAAACTCCTCAT     | 536  |
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| QY | 597  | GCT---GGCAACATGCTAGGCACAGCCTGTGGAGCCCGAGATATGGCCCGCAGAGCTC     | 653  |
| Db | 173  | GlyLysGlyAspValMetSerThrAlaCysGlyThrProGlyTyrValAlaProGluVal   | 192  |
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US-10-355-975A-10  
; Sequence 10, Application US/10355975A

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; Patent No. 6759223
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; INVENTOR: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: CALCIUM/CALMODULIN-DEPENDENT KINASE
; FILE REFERENCE: 2923-B
; CURRENT APPLICATION NUMBER: US/10/355,975A
; PRIORITY FILING DATE: 2003-01-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 355
; TYPE: PRP
; ORGANISM: Mus musculus
US-10-355-975A-10

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Score: 1169.50 Matches: 215
Percent Similarity: 84.78% Conservative: 58
Best Local Similarity: 66.77% Mismatches: 46
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DB: 4 Gaps: 2

US-10-032-254A-1 (1-1554) x US-10-355-975A-10 (1-355)

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; Sequence 4, Application US/09733388
; Patent No. 6602698
; GENERAL INFORMATION:
; APPLICANT: Donoho, Greg
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambowicz, Brian
; APPLICANT: Abuin, Alejandro
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6602698el Human Kinase Proteins and
; FILE REFERENCE: LEX-0103-USA
; CURRENT APPLICATION NUMBER: US/09/733,388
; PRIOR FILING DATE: 2000-12-07
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 356
; TYPE: PRP
; ORGANISM: Homo sapiens
US-09-733-388-4

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US-10-032-254A-1 (1-1554) x US-09-733-388-4 (1-356)

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Job time : 55 secs

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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 6, 2005, 11:58:41 ; Search time 822 Seconds  
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Searched: 1465611 seqs, 345679903 residues

Total number of hits satisfying chosen parameters: 2931222

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pcp.\*
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- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pcp.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

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TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:

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| 3   | 1625   | 56.6  | 343    | 17 | US-10-948-518-89    | Sequence 89, Appli |
| 4   | 1184.5 | 41.2  | 332    | 16 | US-10-664-421-13    | Sequence 13, Appli |
| 5   | 1184.5 | 41.2  | 370    | 9  | US-09-817-181-4     | Sequence 4, Appli  |
| 6   | 1184.5 | 41.2  | 370    | 10 | US-09-769-970-19    | Sequence 19, Appli |
| 7   | 1184.5 | 41.2  | 370    | 14 | US-10-142-356-7     | Sequence 7, Appli  |
| 8   | 1184.5 | 41.2  | 370    | 14 | US-10-300-828-4     | Sequence 4, Appli  |
| 9   | 1184.5 | 41.2  | 370    | 14 | US-10-090-002-4     | Sequence 4, Appli  |
| 10  | 1184.5 | 41.2  | 370    | 14 | US-10-204-041-10    | Sequence 10, Appli |
| 11  | 1184.5 | 41.2  | 370    | 16 | US-10-849-400-6     | Sequence 6, Appli  |
| 12  | 1182.5 | 41.2  | 317    | 14 | US-09-935-464-36    | Sequence 36, Appli |
| 13  | 1182.5 | 41.2  | 317    | 14 | US-10-125-835-36    | Sequence 36, Appli |
| 14  | 1176.5 | 41.0  | 326    | 16 | US-10-664-421-55    | Sequence 55, Appli |
| 15  | 1173.5 | 40.9  | 355    | 15 | US-10-258-106-11    | Sequence 11, Appli |
| 16  | 1173.5 | 40.9  | 357    | 14 | US-10-024-036B-2    | Sequence 2, Appli  |
| 17  | 1173.5 | 40.9  | 357    | 15 | US-10-258-106-2     | Sequence 2, Appli  |
| 18  | 1173.5 | 40.9  | 385    | 10 | US-09-733-388-2     | Sequence 2, Appli  |
| 19  | 1173.5 | 40.9  | 385    | 15 | US-10-446-175-2     | Sequence 2, Appli  |
| 20  | 1173.5 | 40.9  | 385    | 17 | US-10-936-445-2     | Sequence 2, Appli  |
| 21  | 1169.5 | 40.7  | 355    | 14 | US-10-355-975-10    | Sequence 10, Appli |
| 22  | 1157   | 40.3  | 356    | 10 | US-09-733-388-4     | Sequence 4, Appli  |
| 23  | 1157   | 40.3  | 356    | 15 | US-10-446-175-4     | Sequence 4, Appli  |
| 24  | 1157   | 40.3  | 356    | 17 | US-10-936-445-4     | Sequence 4, Appli  |
| 25  | 1065   | 37.1  | 460    | 10 | US-09-935-464-3     | Sequence 3, Appli  |
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| 27  | 1065   | 37.1  | 476    | 9  | US-09-960-643-2     | Sequence 2, Appli  |
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| 29  | 1065   | 37.1  | 476    | 14 | US-10-125-835-5     | Sequence 5, Appli  |
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| 31  | 1017.5 | 35.4  | 326    | 9  | US-09-817-181-2     | Sequence 2, Appli  |
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| 33  | 1017.5 | 35.4  | 326    | 15 | US-10-090-002-2     | Sequence 2, Appli  |
| 34  | 874.5  | 30.4  | 298    | 15 | US-10-220-120-240   | Sequence 240, App  |
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ALIGNMENTS

RESULT 1

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; Sequence 54130, Application US/10425114  
; Publication No. US2004003488A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 54130  
; LENGTH: 484  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:

OTHER INFORMATION: Clone ID: LIB4653-002-F12\_FLI pep  
US-10-425-114-54130

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Percent Similarity: 79.79% Conservative: 9  
Best Local Similarity: 77.94% Mismatches: 63  
Query Match: 62.66% Indels: 35  
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US-10-032-254A-1 (1-1554) x US-10-425-114-54130 (1-484)

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Db 418 roLeuProCysCysLeuSerArgProCysProProArgProAlaLysSerArgGlyGlyA 438
Qy 1371 AACTGAGGAGGTCTTCAAAAGTGGACTTGGGAGCCATCTCTTCCGACACCTTGCACGAACA 1430
Db 438 laGlyArgArgAlaSer-----GlyAlaValPheProAlaArg----- 450
Qy 1431 CATGCATTTGTGGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTGG 1490
Db 451 -----LeuLeuCysAlaSerLeuSerValGlyGlyProAlaCysValMetV 466
Qy 1491 CCCTTTAGTTC 1501
Db 466 alMetAlaPhe 469
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## RESULT 2

US-09-769-970-5  
Sequence 5, Application US/09769970  
Publication No. US20030170219A1  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
Hillman, Jennifer L.  
Corley, Neil C.  
Guesler, Karl G.  
Lal, Preeti  
Goli, Surya K.  
Shah, Purvi  
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN  
KINASES  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/769,970  
FILING DATE: 24-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/272,796

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;
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 343 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PROSNOT06
; CLONE: 827431
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-769-970-5
Alignment Scores:
Pred. No.: 9.13e-121 Length: 343
Score: 1625.00 Matches: 316
Percent Similarity: 93.29% Conservative: 4
Best Local Similarity: 92.13% Mismatches: 23
Query Match: 56.58% Indels: 0
DB: 10 Gaps: 0
US-10-032-254A-1 (1-1554) X US-09-769-970-5 (1-343)
QY 105 ATGTCGTCTGCTCAAGAAACAGACGAGGACATCAGCAGTGTCTATGATGATCCGGGAGAAG 164
DB 1 MetLeuLeuLysLysHisThrGluAspIleSerValTyrGluIleArgGluArg 20
QY 165 CTGGGCTCGGTGCTTCTGAGGTGATGCTGCCAGGAAAGGGCTCTGCTCATCTT 224
DB 21 LeuGlySerGlyAlaPheSerGluValValLeuAlaGlnGluArgGlySerAlaHisLeu 40
QY 225 GTGGCCCTCAAGTGCATTCCCAAGAAACGACTTCGGGCAAGGAGGCCCTGTCGAGAAAT 284
DB 41 ValAlaLeuLysCysIleProLysLysAlaLeuArgGlyLysGluAlaLeuValGluAsn 60
QY 285 GAGATCGGGTACTTCGAGAAATCAGCATCCCAACATTTGGTCTCTGGAGAGCTCCAT 344
DB 61 GluIleAlaValLeuArgArgIleSerHisProAsnIleValAlaLeuGluAspValHis 80
QY 345 GAGATGCTTCTCATCTTACTTGGCCATGAGCTGGTAACAGGTGGTGAACCTTTTGAC 404
DB 81 GluSerProSerHisLeuTyrLeuAlaMetGluLeuValThrGlyGlyGluLeuPheAsp 100
QY 405 CGCATCATGAGCGGGCTCTACACAGAGAGAGCCGACCCACCTGTAGGCGAGGTC 464
DB 101 ArgIleMetGluArgGlySerTyrThrGluLysAspAlaSerHisLeuValGlyGlnVal 120
QY 465 CTGGCGCTGCTCTACCTTATAGCTGGGATCGTGCAACCGGACCTCAAGCCTGAA 524
DB 121 LeuGlyAlaValSerTyrLeuHisSerLeuGlyIleValHisArgAspLeuLysProGlu 140
QY 525 AACCTCTCTATGCCACACCTTTTGGAGACTCCAGATCATGGTCTCTGACTTTGGGCTG 584
DB 141 AsnLeuLeuTyrAlaThrProPheGluAspSerLysIleMetValSerAspPheGlyLeu 160
QY 585 TCCAAATACAGCTGCAACATCTAGGACACGCTGTGGACCCAGGATATGTGGCC 644
DB 161 SerLysIleGlnAlaGlyAsnMetLeuGlyThrAlaCysGlyThrProGlyTyrValAla 180
QY 645 CCAGAGCTCTCGGAGCAGAAACCTTACGGGAAGCCGTAGATGTGTGGCCCTGGGTGTC 704
DB 181 ProGluLeuLeuGluGlnLysProTyrGlyLysAlaValAspValIlePheGlyVal 200
QY 705 ATCTCTACATCTCTGCTGTGTGGGTACCCCTCTTATGATGAGAGCGATCTCTGAATC 764
DB 1 IleSerTyrIleLeuLeuCysGlyTyrProProPheTyrIlePheGluSerAspProGluLeu 220
QY 765 TTCAGCCAGATTTCTGAGGCGCAGCTATGAGTTTGAATCCCTTTTGGGATGACATCTCA 824
DB 221 PheSerGlnIleLeuArgAlaSerTyrGluPheAsp***ProPheTyrAspAspIleSer 240
QY 825 GAATCAGCCAAAGACTTCATTCGCCACCTTCTGGAACGTGATCCCCAGAGAGGTTTCAAC 884
DB 241 GluSerGlyLysAspPheIleArgHisLeuLeuGluArgAspLeuGlnLysArgPheThr 260
QY 885 TGCCAGCAGCGCCCTACAGCATCTTTGGATCTCTGGGATGCAGCTTCGATAGGACATC 944
DB 261 CysGlnGlnAlaLeuArgAspLeuTrpIlePheTrpAspThrGlyPheGlyArgAspIle 280
QY 945 CTGGTCTCTGTCAGTGACAGATCCACAGAAATTTTCCAGGACCCCACTGGAAACGTCGA 1004
DB 281 LeuGlyPheValSerGluGlnIleArgLysAsnPheAlaTrpThrHisTrpLysArgAla 300
QY 1005 TTCATGCCACATCTTCCTACGTACATCGTCACATCGTAAAGCTGGGACAAAGCCAGAGGGTGAG 1064
DB 301 PheAsnAlaThrLeuPheLeuArgHisIleArgLysLeuGlyGlnIleProGluGlyGlu 320
QY 1065 GAGSCCTCCAGGAGTGTATGACCCGTCATAGCCACCCAGGCTTGGGACTAGCCAGTCC 1124
DB 321 GlyAlaSerGluGlnGlyMet***ArgHisSerHis***GlyLeuArgAlaGlyGlnPro 340
QY 1125 CCCAAGTGG 1133
DB 341 ProLysTrp 343
RESULT 3
US-10-948-518-89
; Sequence 89, Application US/10948518
; Publication No. US20050064492A1
; GENERAL INFORMATION:
; APPLICANT: FREDERIC J. DESAUVAGE
; APPLICANT: GRETCHEN FRANTZ
; APPLICANT: KENNETH J. HILLAN
; APPLICANT: PAUL POLAKIS
; APPLICANT: ANDREW POLSON
; APPLICANT: VICTORIA SMITH
; APPLICANT: SUSAN D. SPENCER
; APPLICANT: THOMAS D. WU
; APPLICANT: ZEMIN ZHANG
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P5026R1-US
; CURRENT APPLICATION NUMBER: US/10/948,518
; CURRENT FILING DATE: 2004-09-22
; PRIOR APPLICATION NUMBER: US/10/643,795
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/413,192
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US 60/419,008
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/426,847
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/484,959
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 89
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: 233, 328, 333
; OTHER INFORMATION: Unknown amino acid
US-10-948-518-89
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Alignment Scores:
Pred. No.:          9,13e-121      Length:      343
Score:             1625.00         Matches:    316
Percent Similarity: 93.29%         Conservative: 4
Best Local Similarity: 92.13%      Mismatches: 23
Query Match:       56.58%         Indels:     0
DB:                17             Gaps:       0

US-10-032-254A-1 (1-1554) x US-10-948-518-89 (1-343)
QY 105 ATGCTGCTGCTCAGAACAGCGGAGCATCAGCAGTGTCTATGAGATCCGGGAGAG 164
DB 1 MetLeuLeuLeuLysHisThrGluAspIleSerValTyrGluIleArgGluArg 20
QY 165 CTGGGCTCGGGTCTCTCTGAGGTGATCGTCCCGAGAAAGGGCTCTGCTCATCTT 224
DB 21 LeuGlySerGlyAlaPheSerGluValIleLeuAlaGlnGluArgGlySerAlaHisLeu 40
QY 225 GTGGCCCTCAAGTGCATCCCAAGAACGACTTCGGGGCAAGAGGCCCTGGTGGAGAT 284
DB 41 ValAlaLeuLysCysIleProLysLysAlaLeuArgGlyLysGluAlaLeuValGluAsn 60
QY 285 GAGATCGCGTACTTCCGAGAATCAGCCATCCCAACATTGGCTCTGGAGGAGCTCCAT 344
DB 61 GluIleAlaValLeuArgArgIleSerHisProAsnIleValAlaLeuGluAspValHis 80
QY 345 GAGAGTCTTCTCATCTCTACTTGGCCATGAGCTGGTAACAGGTGGTGAACCTTTTAC 404
DB 81 GluSerProSerHisLeuTyrLeuAlaMetGluLeuValThrGlyGlyGluLeuPheAsp 100
QY 405 CGCATATGAGCGGGCTCTCTACAGAGAACGACCCGACCTTGTAGGCGAGGTC 464
DB 101 ArgIleMetGluArgGlySerTyrThrGluLysAspAlaSerHisLeuValGlyGlnVal 120
QY 465 CTTGGCGCTGCTCCTACCTCATAGCTGGCATCGTGACCGGAGCCTCAAGCCTGAA 524
DB 121 LeuGlyAlaValSerTyrLeuHisSerLeuGlyIleValHisArgAspLeuLysProGlu 140
QY 525 AACCTCTCTATGCGACACCTTTTGGAGACTCCCAAGATCATGTCTCTGACTTTGGCTG 584
DB 141 AsnLeuLeuTyrAlaThrProPheGluAspSerLysIleMetValSerAspPheGlyLeu 160
QY 585 TCCAAATACAACTGGCAACATGCTAGGACACGCTGTGGGACCCAGAGATATGTGGCC 644
DB 161 SerLysIleGlnAlaGlyAsnMetLeuGlyThrAlaCysGlyThrProGlyTyrValAla 180
QY 645 CCAGAGCTCTCGGAGCAGAACCTTACGGGAAGCCGTAGATGCTGGGCCCTGGGTGC 704
DB 181 ProGluLeuLeuGluGlnLysProTyrGlyLysAlaValAspValTrpAlaLeuGlyVal 200
QY 705 ATCTCCTACATCTCTGCTGTGGGTACCCCTCTCTATGATGAGAGCATCTCTGAACCTC 764
DB 201 IleSerTyrIleLeuLeuCysGlyTyrProPheTyrAspGluSerAspProGluLeu 220
QY 765 TTCAGCCAGATTCAGAGCCGAGCTATGAGTTTGAATCCCTCTTGGATGACATCTCA 824
DB 221 PheSerGlnIleLeuArgAlaSerTyrGluPheAsp***ProPheTyrAspAspIleSer 240
QY 825 GAATCAGCCAAAGACTTCATTCGCCACCTCTGGACGTCGATCCCGAGAGAGGTTCCAC 884
DB 241 GluSerGlyLysAspPheIleArgHisLeuLeuGluArgAspLeuGlnLysArgPheThr 260
QY 885 TGCCAGAGGCGCTACAGCATCTTTGGATCTCTGGGATGACGCTTCGATAGGAGCATC 944
DB 261 CysGlnGlnAlaLeuArgAspLeuTrpIlePheTrpAspThrGlyPheGlyArgAspIle 280
QY 945 CTGGGTTCTGTGAGTGCAGATCCAGAAATTTTGGCAGACCCACTGGAAAGGCTGCA 1004
DB 281 LeuGlyPheValSerGluGlnIleArgLysAsnPheAlaTrpThrHisTrpLysArgAla 300
QY 1005 TTCATGCCCATCATTCCTACGTCACATCCGTAAGCTGGGACCAAGCCAGAGGGTGAG 1064
DB 1105 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuTyrTyr 150

301 PheAsnAlaThrLeuPheLeuArgHisIleArgLysLeuGlyGlnIleProGluGlyGlu 320
1065 GAGGCTCCAGGAGTGTATGACCCGTATAGCCACCCAGGCTTGGGACTAGCCAGTCC 1124
321 GlyAlaSerGluGlnGlyMet***ArgHisSerHis**GlyLeuArgAlaGlyGlnPro 340
1125 CCCAAGTGG 1133
341 ProLysTrp 343

RESULT 4
US-10-664-421-13
; Sequence 13, Application US/10664421
; Publication No. US20040142864A1
; GENERAL INFORMATION:
; APPLICANT: BREMER, RYAN
; APPLICANT: IBRAHIM, PRABHA
; APPLICANT: KUMAR, ABHINAV
; APPLICANT: MANDIYAN, VALSAN
; APPLICANT: MILBURN, MICHAEL V.
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
; FILE REFERENCE: 039363/0703
; CURRENT APPLICATION NUMBER: US/10/664,421
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-664-421-13

Alignment Scores:
Pred. No.:          1,28e-85      Length:      332
Score:             1184.50         Matches:    220
Percent Similarity: 85.17%         Conservative: 50
Best Local Similarity: 69.40%      Mismatches: 44
Query Match:       41.24%         Indels:     3
DB:                16             Gaps:       2

US-10-032-254A-1 (1-1554) x US-10-664-421-13 (1-332)
QY 120 AAACAGACGGAGACATCAGCAGTGTCTATGATCCGGGAGAGCTGGGCTCGGTGCC 179
DB 11 LysGlnAlaGluAspIleArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla 30
QY 180 TTCTCTGAGTGTGTCGGCCAGGAAAGGGGCTCTGCTCATCTTGTGGCCCTCAAGTGC 239
DB 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50
QY 240 ATTCCCAAGAACACTTCGGGCGAGGAGCCCTGGTGAGATGAGATCGCGGTACTT 299
DB 51 IleAlaLysLysAlaLeuGluGlyLysGluGlySerMetGluAsnGluIleAlaValLeu 70
QY 300 CGCAGATCAGCATCCCAACATTGTGCTCTGAGGACGCTCCATGAGAGTCTTCTCAT 359
DB 71 HisLysIleLysHisProAsnIleValAlaLeuAspAspIleTyrGluSerGlyGlyHis 90
QY 360 CTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTGTTGACCCGATCATGAGCGG 419
DB 91 LeuTyrLeuIleMetGlnLeuValSerGlyGlyLeuPheAspArgIleValGluLys 110
QY 420 GGCTCTCTACACAGAGGAGCCAGCCACCTTGTAGGGCAGGCTCTTGGGCTGTCTCC 479
DB 111 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130
QY 480 TACCTTCATAGCTGGGCTGTCGACCGGAGCCTCAAGCCTGAAACCTCTCTATGCC 539
DB 131 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuTyrTyr 150
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QY 540 ACACCTTTGGAGCTCCAGATCATGCTCTGACTTTGGCTGTCCAAATACAA--- 596
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Db 151 SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp 170
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QY 597 GCTGCAACATGCTAGGACAGCTCTGGGACCCAGATATGTCGCCAGAGCTCTG 656
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Db 171 ProGlySerValLeuSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeu 190
   ::::|||||
QY 657 GAGCAGAAACCTACGGAGCCCTAGATGTGTGGCCCTGGGTCTCATCTCTACATC 716
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Db 191 AlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyrIle 210
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QY 717 CTGCTGTGTGGGTACCCCTTCTATCATGAGAGCGATCTCTGAACTCTTTCAGCCAGATT 776
   ::::|||||
Db 211 LeuLeuCysGlyTyrProProPheTyrAspGluAsnAspAlaLysLeuPheGluGlnIle 230
   ::::|||||
QY 777 CTGAGGCGCAGCTATGAGTTGACTCCCTTTGGGATGATCCAGAGAGTTTCCAGTCCAGGCC 836
   ::::|||||
Db 231 LeuLysAlaGluTyrGluPheAspSerProTyrTrpAspPheGlyLeuSerLysMetGluAsp 250
   ::::|||||
QY 837 GACTTCATCCCACTCTCGAAGCTGATCCAGAGAGTTTCCAGTCCAGGCC 896
   ::::|||||
Db 251 AspPheIleArgHisLeuMetGluLysAspProGluLysArgPheThrCysGluGlnAla 270
   ::::|||||
QY 897 CTACAGCATCTTGGATCTCTGGGATGCGACCTTTCGATAGGAGCATCTCTGGGTCTGTC 956
   ::::|||||
Db 271 LeuGlnHisProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyrIle 290
   ::::|||||
QY 957 AGTGAGCAGATCCAGAAAGTTTGGCAGGCCCTGGAAGCGGTGCATTCATGCGCCACA 1016
   ::::|||||
Db 291 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 310
   ::::|||||
QY 1017 TCATTCTACCTCAGTCCGTAAG-----CTGGGACAAAGCCAGAGGT 1061
   ::::|||||
Db 311 AlaValValArgHisMetArgLysLeuGlnLeuGlyHisGlnProGlyGly 327

RESULT 5
US-09-817-181-4
; Sequence 4, Application US/09817181
; Patent No. US20020142427A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001189
; CURRENT APPLICATION NUMBER: US/09/817,181
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Human
US-09-817-181-4

Alignment Scores:
Pred. No.: 1.32e-85 Length: 370
Score: 1184.50 Matches: 220
Percent Similarity: 85.53% Conservative: 52
Best Local Similarity: 69.18% Mismatches: 43
Query Match: 41.24% Indels: 3
DB: 9 Gaps: 2

US-10-032-254A-1 (1-1554) x US-09-817-181-4 (1-370)

QY 120 AAACGACGGAGGACATCAGAGTGTCTATGAGATCCGGGAGAGCTGGGTCTGGGTGCC 179
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Db 11 LysGlnAlaGluAspIleArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla 30
   ::::|||||
QY 180 TTCTCTGAGGTGATGCTGCGCCAGAAAGGGCTCTGCTCATCTTGTGGCCCTCAAGTGC 239
   ::::|||||
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Db 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50
QY 240 ATTCCTCCAGAAAGCAGCTTCGGGGCAAGAGAGCCCTGGTGGAGATGAGATCGCGTACTT 299
   ::::|||||
Db 51 IleAlaLysGluAlaLeuGluGlySerMetGluAsnGluIleAlaValLeu 70
   ::::|||||
QY 300 CGCAGATTCAGCCATCCCAACATTTGGCTCTGGAGAGCGTCCATGAGAGTCTTCTCAT 359
   ::::|||||
Db 71 HisLysIleLysHisProAsnIleValAlaLeuAspAspIleTyrGluSerGlyGlyHis 90
   ::::|||||
QY 360 CTCTACTTGGCCATGGAGCTGTTAACAGTGGTGAACCTGTTGACCGCATCATGGAGCGG 419
   ::::|||||
Db 91 LeuTyrLeuIleMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGluLys 110
   ::::|||||
QY 420 GGCTCTTACACAGAAAGAGCAGCCAGCCACTTGTAGGGCAGGTCCTTGGCGCTGTCTCC 479
   ::::|||||
Db 111 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130
   ::::|||||
QY 480 TACCTTTCATAGCTGGGCATCGTCACGGGACCTCAAGCCTGAAACCTCTCTATGCC 539
   ::::|||||
Db 131 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuTyrTyr 150
   ::::|||||
QY 540 ACACCTTTTGGAGCTCCAGATCATGCTCTGACTTTGGCCCTGTCCAAATACAA--- 596
   ::::|||||
Db 151 SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp 170
   ::::|||||
QY 597 GCTGCAACATGCTAGGACAGCTCTGGGACCCAGATATGTCGCCAGAGCTCTG 656
   ::::|||||
Db 171 ProGlySerValLeuSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeu 190
   ::::|||||
QY 657 GAGCAGAAACCTACGGGAGCGCTAGATGTGTGGCCCTGGGTGTCTCATCTCTACATC 716
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Db 191 AlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyrIle 210
   ::::|||||
QY 717 CTGCTGTGTGGGTACCCCTTCTATCATGAGAGCGATCTCTGAACTCTTTCAGCCAGATT 776
   ::::|||||
Db 211 LeuLeuCysGlyTyrProProPheTyrAspGluAsnAspAlaLysLeuPheGluGlnIle 230
   ::::|||||
QY 777 CTGAGGCGCAGCTATGAGTTGACTCCCTTTGGGATGATCATCTCAGATCAGCCAAA 836
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Db 231 LeuLysAlaGluTyrGluPheAspSerProTyrTrpAspPheGlyLeuSerAspSerAlaLys 250
   ::::|||||
QY 837 GACTTCATTCGCCACTCTCGAAGCTGATCCCGAGAGAGTTTCCAGTCCAGGCC 896
   ::::|||||
Db 251 AspPheIleArgHisLeuMetGluLysAspProGluLysArgPheThrCysGluGlnAla 270
   ::::|||||
QY 897 CTACAGCATCTTGGATCTCTGGGATGCGACCTTTCGATAGGAGCATCTCTGGGTCTGTC 956
   ::::|||||
Db 271 LeuGlnHisProTyrTrpIleAlaGlyAspThrAlaLeuAspLysAsnIleHisGlnSerVal 290
   ::::|||||
QY 957 AGTGAGCAGATCCAGAAAGTTTGGCAGGCCCTGGAAGCGGTGCATTCATGCGCCACA 1016
   ::::|||||
Db 291 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 310
   ::::|||||
QY 1017 TCATTCTACCTCAGTCCGTAAG-----CTGGGACAAAGCCAGAGGTGAG 1064
   ::::|||||
Db 311 AlaValValArgHisMetArgLysLeuGlnLeuGlyThrSerGlnGluGlyGln 328

RESULT 6
US-09-769-970-19
; Sequence 19, Application US/09769970
; Publication No. US20030170219A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Hillman, Jennifer L.
; Corley, Neil C.
; Guegler, Karl G.
; Lai, Preeti
; Goli, Surya K.
; Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; KINASES
; NUMBER OF SEQUENCES: 21
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Db 11 LysGlnAlaGluAspIleArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla 30
Qy 180 TTCTCTGAGGTGATGTCGGCCAGAAAGGGCTCTGCTCATCTTGTGGCCCTCAAGTGC 239
Db 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50
Qy 240 ATTCCCAAGAAGACACTTCGGGCAAGGAGCCCTGTGGAGATGATGCGGTACTT 299
Db 51 IleAlaLysGluAlaLeuGluGlyLysGlySerMetGluAenGluIleAlaValLeu 70
Qy 300 CGCAGATATCCCAATCCCAATCTGTGCTGAGGACGTCCTGAGAGTCTTCTCAT 359
Db 71 HisLysIleLysHisProAsnIleValAlaLeuAspIleTyrGluSerGlyHis 90
Qy 360 CTCTACTTGGCCATGAGCTGGTAAACAGGTGGTGAACCTTGTGACCCCATCATGAGCGG 419
Db 91 LeuTyrLeuIleMetGlnLeuValSerGlyGlyLeuPheAspArgIleValGluLys 110
Qy 420 GGCTCTTACACAGAGAAGGAGCCAGCCACCTTGTAGGGCAGGTCTTGGCGTCTCTCC 479
Db 111 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130
Qy 480 TACCTTCTATGAGCTGGGATCGTCACCGGACCTCAAGCTGAAACCTCTCTATGCC 539
Db 131 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAenLeuTyrTyr 150
Qy 540 ACACCTTTTGGAGTCTCAAGATCATGCTCTGACTTTGGCTGTGCTCAAAATACAA--- 596
Db 151 SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp 170
Qy 597 GCTGGCAACCTGAGGACAGCTGTGGGACCCAGGATATGTGGCCCTGATGTCTCTATGC 656
Db 171 ProGlySerValLeuSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeu 190
Qy 657 GAGCAGAAACCTACGGGAGGCGGTAGATGTGGCCCTGATGTCTCTATGCATC 716
Db 191 AlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyrIle 210
Qy 717 CTGTGTGTGGTATCCCTCTTATGATGAGAGCATCTGAACTCTTCCAGCAGATT 776
Db 211 LeuLeuCysGlyTyrProPheTyrAspGluAsnAspAlaLysLeuPheGluGlnIle 230
Qy 777 CTGAGGCGCAGTATGATGTTGATCTTGGGACCCAGGATATGTGGCCCTGATGTCTCT 836
Db 231 LeuLysAlaGluTyrGluPheAspSerProTyrTrpAspIleSerAspSerAlaLys 250
Qy 837 GACTTCACTTCCACCTTCTGACCTGATGTCACGAGAGGTTTCACTGCGCAGCGCC 896
Db 251 AspPheIleArgHisLeuMetGluLysAspProGluLysArgPheThrCysGluGlnAla 270
Qy 897 CTACAGCATCTTGGATCTCTGGGATGTCAGCTTTCAGTGGGACATCTCTGGGTCTGTC 956
Db 271 LeuGlnHisProTyrIleAlaGlyAspThrAlaLeuAspLysAsnIleHisGlnSerVal 290
Qy 957 AGTGAGCAGATCCAGAGAATTTTGGCAGGACCCACTGGAAGCGGTGATTCATTCAGCACA 1016
Db 291 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 310
Qy 1017 TCATTCTTACATCCCTGTAAG-----CTGGGCAAGGCCAGGAGGTGAG 1064
Db 311 AlaValValArgHisMetArgLysLeuGlnLeuGlyThrSerGlnGluGlyGln 328
RESULT 8
US-10-300-828-4
; Sequence 4, Application US/10300828
; Publication No. US2003007799A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001189CON
; CURRENT APPLICATION NUMBER: US/10/300,828
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; CURRENT FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Human
; US-10-300-828-4
Alignment Scores:
Pred. No.: 1.32e-85 Length: 370
Score: 1184.50 Matches: 220
Percent Similarity: 85.53% Conservative: 52
Best Local Similarity: 69.18% Mismatches: 43
Query Match: 41.24% Indels: 3
DB: 14 Gaps: 2
US-10-032-254A-1 (1-1554) x US-10-300-828-4 (1-370)
Qy 120 AACACAGCGAGGACATCAGCAGTGTCTATGAGATCCGGAGAGCTGGGCTCGGTGCC 179
Db 11 LysGlnAlaGluAspIleArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla 30
Qy 180 TTCTCTGAGGTGATGTCGGCCAGGAAAGGGCTCTGCTCATCTTGTGGCCCTCAAGTGC 239
Db 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50
Qy 240 ATTCCCAAGAAGACACTTCGGGCAAGGAGCCCTGTGGAGATGATGATGCGGTACTT 299
Db 51 IleAlaLysGluAlaLeuGluGlyLysGlySerMetGluAenGluIleAlaValLeu 70
Qy 300 CGCAGATATCCCAATCCCAATCTGTGCTCTGAGGACGTCCTCATGAGAGTCTTCTCAT 359
Db 71 HisLysIleLysHisProAsnIleValAlaLeuAspIleTyrGluSerGlyHis 90
Qy 360 CTCTACTTGGCCATGAGCTGGTAAACAGGTGGTGAACCTTGTGACCCCATCATGAGCGG 419
Db 91 LeuTyrLeuIleMetGlnLeuValSerGlyGlyLeuPheAspArgIleValGluLys 110
Qy 420 GGCTCTTACACAGAGAAGGAGCCAGCCACCTTGTAGGGCAGGTCTTGGCGTCTCTCC 479
Db 111 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130
Qy 480 TACCTTCTATGAGCTGGGATCGTCACCGGACCTCAAGCTGAAACCTCTCTATGCC 539
Db 131 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAenLeuTyrTyr 150
Qy 540 ACACCTTTTGGAGTCTCAAGATCATGCTCTGACTTTGGCTGTGCTCAAAATACAA--- 596
Db 151 SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp 170
Qy 597 GCTGGCAACCTGAGGACAGCTGTGGGACCCAGGATATGTGGCCCTGATGTCTCTATGC 656
Db 171 ProGlySerValLeuSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeu 190
Qy 657 GAGCAGAAACCTACGGGAGGCGGTAGATGTGGCCCTGATGTCTCTATGCATC 716
Db 191 AlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyrIle 210
Qy 717 CTGTGTGTGGTATCCCTCTTATGATGAGAGCATCTGAACTCTTCCAGCAGATT 776
Db 211 LeuLeuCysGlyTyrProPheTyrAspGluAsnAspAlaLysLeuPheGluGlnIle 230
Qy 777 CTGAGGCGCAGTATGATGTTGATCTTGGGACCCAGGATATGTGGCCCTGATGTCTCT 836
Db 231 LeuLysAlaGluTyrGluPheAspSerProTyrTrpAspIleSerAspSerAlaLys 250
Qy 837 GACTTCACTTCCACCTTCTGACCTGATGTCACGAGAGGTTTCACTGCGCAGCGCC 896
Db 251 AspPheIleArgHisLeuMetGluLysAspProGluLysArgPheThrCysGluGlnAla 270
Qy 897 CTACAGCATCTTGGATCTCTGGGATGTCAGCTTTCAGTGGGACATCTCTGGGTCTGTC 956
Db 271 LeuGlnHisProTyrIleAlaGlyAspThrAlaLeuAspLysAsnIleHisGlnSerVal 290
Qy 957 AGTGAGCAGATCCAGAGAATTTTGGCAGGACCCACTGGAAGCGGTGATTCATTCAGCACA 1016
Db 291 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 310
Qy 1017 TCATTCTTACATCCCTGTAAG-----CTGGGCAAGGCCAGGAGGTGAG 1064
Db 311 AlaValValArgHisMetArgLysLeuGlnLeuGlyThrSerGlnGluGlyGln 328
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Db 271 LeuGlnHisProTrrpIleAlaGlyAspThrAlaLeuAspLysAsnIleHisGlnSerVal 290  
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Db 291 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 310  
Qy 1017 TCATTCTCAGTGCATCCGTAAG-----CTGGACAAAGCCACAGAGGTGAG 1064  
Db 311 AlaValValArgHisMetArgLysLeuGlnLeuGlyThrSerGlnGluGlyGln 328  
RESULT 9  
US-10-090-002-4  
; Sequence 4, Application US/10090002  
; Publication No. US20030175926A1  
; GENERAL INFORMATION:  
; APPLICANT: YAN, Chunhua et al.  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001316  
; CURRENT APPLICATION NUMBER: US/10/090\_002  
; CURRENT FILING DATE: 2002-03-08  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-090-002-4  
Alignment Scores:  
Pred. No.: 1.32e-85 Length: 370  
Score: 1184.50 Matches: 220  
Percent Similarity: 85.53% Conservative: 52  
Best Local Similarity: 69.18% Mismatches: 43  
Query Match: 41.24% Indels: 3  
DB: 14 Gaps: 2  
US-10-032-254A-1 (1-1554) x US-10-090-002-4 (1-370)

Qy 120 AAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAGCTGGGTCGGGTGCC 179  
Db 11 LysGlnAlaGluAspIleArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla 30  
Qy 180 TTCTCTGAGTGTATGTCGGCCAGAGAAAGGGCTCTGCTCATCTGTGGCCCTCAAGTGC 239  
Db 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50  
Qy 240 ATTCCTCAAGAACACTTCGGGGCAGGAGCCCTGTGGAGATGAGATCGCGTACTT 299  
Db 51 IleAlaLysGluAlaLeuGluGlyLysGluGlySerMetGluAsnGluIleAlaValLeu 70  
Qy 300 CGCAGAAATCAGCCATCCCAACATGTGGCTCTGAGGAGCGTCCATGAGATCTCTCAT 359  
Db 71 HisLysIleLysHisProAsnIleValAlaLeuAspIleTyrGluSerGlyGlyHis 90  
Qy 360 CTCTACTTGGCCATCGAGCTGTTAACAGGTGGTGAACCTTTTGACCGCATCATGAGCGG 419  
Db 91 LeuTyrLeuIleMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGluLys 110  
Qy 420 GGCTCTACACAGAGAGGAGCCAGCCACTTGTAGGGCAGGTCTTGGCGCTGTCTCC 479  
Db 111 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130  
Qy 480 TACCTTCATACCTGGGCATCGTCACCGGACCTCAAGCCCTGAAACCTCTCTATGCC 539  
Db 131 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuLeuTyrTyr 150  
Qy 540 ACACCTTTTGGAGCTCCCAAGATCATGTCTCTGACTTTTGGCCCTGTCCAAATACAA--- 596  
Db 151 SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp 170  
Qy 597 GCTGCCACATGCTAGGCACAGCCCTGTGGACCCAGGATATGTGGCCCGCAGAGCTCTG 656

Db 171 ProGlySerValLeuSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeu 190  
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Db 191 AlaGlnLysProTrrpLysSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyrIle 210  
Qy 717 CTGCTGTGGGTACCCCTCTTATGATGAGAGGATCCTGAACTCTTCAGCCAGATT 776  
Db 211 LeuLeuCysGlyTyrProPheTyrAspGluAsnAspAlaLysLeuPheGluGlnIle 230  
Qy 777 CTGAGGCGCAGCTATCAGTTTGACTCCCTCTTGGGATGACATCTCAGAATCAGCCAAA 836  
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Qy 837 GACTTCATTCCGCCACCTCTCGGAACCTGATCCCGACAGAGGTTCACCTCCAGCAGGCC 896  
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Qy 957 AGTGACAGATCCAGAAGAAATTTTGCAGGACCCACCTGGGAAGCGTGCATTCAATGCCACA 1016  
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Qy 1017 TCATTCTCAGTGCATCCGTAAG-----CTGGACAAAGCCCGAGGGTGTAG 1064  
Db 311 AlaValValArgHisMetArgLysLeuGlnLeuGlyThrSerGlnGluGlyGln 328  
RESULT 10  
US-10-204-041-10  
; Sequence 10, Application US/10204041  
; Publication No. US20030176443A1  
; GENERAL INFORMATION:  
; APPLICANT: STEIN-GERLACH, MATTHIAS  
; APPLICANT: SALASSIDIS, KONSTADINOS  
; APPLICANT: BACHER, STEFAN  
; TITLE OF INVENTION: Pyridylpyrimidine Derivatives as Effective Compounds Against Prio  
; TITLE OF INVENTION: Infections and Prion Diseases  
; FILE REFERENCE: AXM-007.1P US  
; CURRENT APPLICATION NUMBER: US/10/204\_041  
; CURRENT FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: EP 01111858.5  
; PRIOR FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: PCT/EP02/05420  
; PRIOR FILING DATE: 2002-05-16  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-204-041-10  
Alignment Scores:  
Pred. No.: 1.32e-85 Length: 370  
Score: 1184.50 Matches: 220  
Percent Similarity: 85.53% Conservative: 52  
Best Local Similarity: 69.18% Mismatches: 43  
Query Match: 41.24% Indels: 3  
DB: 14 Gaps: 2  
US-10-032-254A-1 (1-1554) x US-10-204-041-10 (1-370)  
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Db 11 LysGlnAlaGluAspIleArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla 30  
Qy 180 TTCTCTCAGTGTATGTCGGCCAGAGAAAGGGCTCTGCTCATCTGTGGCCCTCAAGTGC 239  
Db 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50  
Qy 240 ATTCCTCAAGAACACTTCGGGGCAGGAGCCCTGTGGAGATGAGATCGCGTACTT 299  
Db 51 IleAlaLysGluAlaLeuGluGlyLysGluGlySerMetGluAsnGluIleAlaValLeu 70  
Qy 300 CGCAGAAATCAGCCATCCCAACATGTGGCTCTGAGGAGCGTCCATGAGATCTCTCAT 359  
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Qy 360 CTCTACTTGGCCATCGAGCTGTTAACAGGTGGTGAACCTTTTGACCGCATCATGAGCGG 419  
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Qy 420 GGCTCTACACAGAGAGGAGCCAGCCACTTGTAGGGCAGGTCTTGGCGCTGTCTCC 479  
Db 111 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130  
Qy 480 TACCTTCATACCTGGGCATCGTCACCGGACCTCAAGCCCTGAAACCTCTCTATGCC 539  
Db 131 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuLeuTyrTyr 150  
Qy 540 ACACCTTTTGGAGCTCCCAAGATCATGTCTCTGACTTTTGGCCCTGTCCAAATACAA--- 596  
Db 151 SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp 170  
Qy 597 GCTGCCACATGCTAGGCACAGCCCTGTGGACCCAGGATATGTGGCCCGCAGAGCTCTG 656

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Db 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50
Qy 240 ATCCCAAGAAAGACATTCGGGGCAAGAGGCCCTGGTGGAGATGAGATCGCGGTACTT 299
Db 51 IleAlaLysGluAlaLeuGluGlyLysGlySerMetGluAsnGluIleAlaValLeu 70
Qy 300 CGCAGATCAGCCATCCACATTTGGCTGTGGAGAGCGTCCATGAGATCTTCAT 359
Db 71 HisLysIleLysHisProAsnIleValAlaLeuAspAspIleTyrGluSerGlyGlyHis 90
Qy 360 CTCTACTTGGCCATGGAGCTGTTAACAGAGTGGTCAACTGTTGACCCCATCATCGAGCGG 419
Db 91 LeuTyrLeuIleMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGluLys 110
Qy 420 GGCTCTTACACAGAGGAGCGCCAGCCATCTTAGCGAGGTCCTTGGCGTGTCTCC 479
Db 111 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130
Qy 480 TACCTTCATAGCTGGGCATCGTGCACCGGACCTCAAGCTGAAACCTCTCTATGCC 539
Db 131 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuTyrTyr 150
Qy 540 ACACCTTTTGGAGCTCCAGATCATGCTCTGACTTTCGCTTGGCTGTCCAAATACAA--- 596
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Db 171 ProGlySerValLeuSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeu 190
Qy 657 GAGCAGAAACCTACGGGAAGCGCGTAGATGTGTGGCCCTGGGTGTCTCTACATC 716
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Qy 717 CTGCTGTGGTGTACCCCTCTTATGATGAGAGCGATCTCTGAACCTCTCAGCCAGATT 776
Db 211 LeuLeuCysGlyTyrProPheTyrAspGluAsnAspAlaLysLeuPheGluGlnIle 230
Qy 777 CTGAGGCCAGCTATGAGTTTGACTCCCTTTGGGATGACATCTCAGAAATCAGCAAA 836
Db 231 LeuLysAlaGluTyrGluPheAspSerProTyrTrpAspIleSerAspSerAlaLys 250
Qy 837 GACTTCATTCGCCACCTTCTGGAAAGCGTATGCTCCCTTTGGGATGACATCTCAGAAATCAGCAAA 896
Db 251 AspPheIleArgHisLeuMetGluLysAspProGluLysArgPheThrCysGluGlnAla 270
Qy 897 CTACAGATCTTTGGATCTCTGGGGATGACGCTTCGATAGGAGACATCTGGGTGTCTGC 956
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Qy 957 AGTGAGCAGATCCAGAGAAATTTGCCAGGACCCACTGGAGCGTGCATTCAATGCCACA 1016
Db 291 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 310
Qy 1017 TCATCTCTACGTCACATCCGTAAG-CTGGGCAAAAGCCCGCAGAGGGGTGAG 1064
Db 311 AlaValAlaArgHisMetArgLysLeuGlnLeuGlyThrSerGlnGluGlyGln 328
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## RESULT 11

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US-10-649-400-6
; Sequence 6, Application US/10649400
; Publication No. US20040110198A1
; GENERAL INFORMATION:
; APPLICANT: Bunney Jr., William E.
; APPLICANT: Jones, Edward G.
; APPLICANT: Molnar, Margherita
; APPLICANT: The Board of Trustees of The Leland Stanford
; APPLICANT: Junior University
; TITLE OF INVENTION: Genes Involved in Neuropsychiatric Disorders
; FILE REFERENCE: 020895-000720US
; CURRENT APPLICATION NUMBER: US/10/649,400
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/406,879
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; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/451,306
; PRIOR FILING DATE: 2003-02-27
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: calcium/calmodulin dependent protein kinase I
; OTHER INFORMATION: (CAMKI)
; US-10-649-400-6
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## Alignment Scores:

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Pred. No.: 1,32e-85 Length: 370
Score: 1184.50 Matches: 220
Percent Similarity: 85.53% Conservative: 52
Best Local Similarity: 69.18% Mismatches: 43
Query Match: 41.24% Indels: 3
Gaps: 2
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US-10-032-254A-1 (1-1554) x US-10-649-400-6 (1-370)

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Qy 180 TTCTCTGAGTGTGCTGGGCCAGGAAAGGGCTCTCTCATCTTGTGGCCCTCAAGTGC 239
Db 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50
Qy 240 ATTCACCAAGAAAGCACATTCGGGGCAAGAGCGCCCTGTGGAGATGAGATCGCGTACTT 299
Db 51 IleAlaLysGluAlaLeuGluGlyLysGlySerMetGluAsnGluIleAlaValLeu 70
Qy 300 CGCAGATCAGCCATCCAAACATTTGGCTGTGGGACCGTCCATGAGAGTCTTCTCAT 359
Db 71 HisLysIleLysHisProAsnIleValAlaLeuAspAspIleTyrGluSerGlyGlyHis 90
Qy 360 CTCTACTTGGCCATGGAGCTGTGTAAACAGTGGTGAACCTGTTTGACCGCATCATCGAGCGG 419
Db 91 LeuTyrLeuIleMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGluLys 110
Qy 420 GGCTCTTACACAGAGAGGAGCGCCAGCCATCTTAGCGAGGTCCTTGGCGTGTCTCC 479
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Qy 480 TACCTTCATAGCTTGGGCATCTGCACCGGACCTCAAGCTGAAACCTCTCTATGCC 539
Db 131 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuTyrTyr 150
Qy 540 ACACCTTTTGGAGCTCCAAAGATCATGCTCTGACTTGTGGCCCTGTCCAAATACAA--- 596
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Db 211 LeuLeuCysGlyTyrProPheTyrAspGluAsnAspAlaLysLeuPheGluGlnIle 230
Qy 777 CTGAGGCCAGCTATGAGTTTGACTCCCTTTGGGATGACATCTCAGAAATCAGCAAA 836
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QY 120 AAACAGCGGAGGACATCAGCAGTGTCTATGAGATCCGGAGAGAGCTGGGCTCGGTGCC 179
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QY 180 TTCTCTGAGGTGATGCTGGGCCAGGAAAGGGCTCTCTCATCTTGTGGCCCTCAAGTGC 239
Db 21 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 40
QY 240 ATTCCCAAGAAAGACATCTTCGGGCAAGAGCGCCCTGGTGAGAAATGAGATCGCGGTACTT 299
Db 41 IleAlaLysGluAlaLeuGluGlyLysGluGlySerMetGluAsnGluIleAlaValLeu 60
QY 300 CGCAGAAATCAGCCATCCCAACATTTGCTGTGGAGACGTCCTCAGAGATCTTCTCAT 359
Db 61 HisLysIleLysHisProAsnIleValAlaLeuAspIleTyrGluSerGlyGlyHis 80
QY 360 CTCTACTTGGCCATCGGAGTGTGAACAGGTGGTGAACCTGTTGACCCGCATCGGAGCGG 419
Db 81 LeuTyrLeuIleMetGlnLeuValSerGlyGlyLysGluLeuPheAspArgIleValGluLys 100
QY 420 GGCTCTTACACAGAGAGGAGCGCCAGCCACCTTCTAGGAGAGTCTTGGCGTGTCTCC 479
Db 101 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 120
QY 480 TACCTTCATAGCTGGGCATCGTCACCGGACCTCAAGCTGAAACCTCTCATATGCC 539
Db 121 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuLeuTyrTyr 140
QY 540 ACACCTTTTGAGGACTCCAGATCATGCTCTGACTTTGGCTGTGCTCCAAATAACA--- 596
Db 141 SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp 160
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Db 161 ProGlySerValLeuSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeu 180
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Db 181 AlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyrIle 200
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Db 201 LeuLeuCysGlyTyrProPheTyrAspGluAsnAlaLysLeuPheGluGlnIle 220
QY 777 CTGAGGCCAGCTATGATTTGACTCCCTCTTGGATGACATCTCAGAAATCAGCAAA 836
Db 221 LeuLysAlaGluTyrGluPheAspSerProTyrTrpAspIleSerAspSerAlaLys 240
QY 837 GACTTCATTCGCCACCTTCTGGACGTGATCCCGAGAGAGGTTTCACCTGCCAGCGCC 896
Db 241 AspPheIleArgHisLeuMetGluLysAspProGluLysArgPheThrCysGluGlnAla 260
QY 897 CTACAGCATCTTTGGATCTCTGGGGATCGACGCTTCGATAGGAGCATCCTGGGTCTGTC 956
Db 261 LeuGlnHisProTyrIleAlaGlyAspThrAlaLeuAspLysAsnIleHisGlnSerVal 280
QY 957 AGTGAGCAGATCCAGAGAATTTGCCAGGACCCACTGGAGCGTGTGATTCATTCACCA 1016
Db 281 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 300
QY 1017 TCATTCTACGTACATCCCTGAAG-----CTGGGCAAAAGCCAGAGGTT 1061
Db 301 AlaValValArgHisMetArgLysLeuGlnLeuGlyThrSerGlnGluGly 317
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## RESULT 14

US-10-664-421-55

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; Sequence 55, Application US/10664421
; Publication No. US20040142864A1
; GENERAL INFORMATION:
; APPLICANT: BREMER, RYAN
; APPLICANT: IBRAHIM, PRABHA
; APPLICANT: KUMAR, ABHINAV
; APPLICANT: MANDIYAN, VALSAN
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; APPLICANT: MILBURN, MICHAEL V.
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
; FILE REFERENCE: 039363/0703
; CURRENT APPLICATION NUMBER: US/10/664,421
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 55
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-664-421-55
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Alignment Scores: 5.53e-85 Length: 326
Pred. No.: 1176.50 Matches: 221
Score: 1176.50 Conservative: 51
Percent Similarity: 81.19% Mismatches: 42
Best Local Similarity: 65.97% Indels: 21
Query Match: 40.96% Gaps: 2
DB: 16
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US-10-032-254A-1 (1-1554) x US-10-664-421-55 (1-326)

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Db 111 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130
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Db 313 ThrAlaValValArgHisMetArgLysLeuHisLeuGlySerSerLeuAspSerSerAsn 332  
Qy 1068 GCCTCC 1073  
Db 333 AlaSer 334

Search completed: June 6, 2005, 12:58:39  
Job time : 831 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 5, 2005, 22:42:05 ; Search time 10887 Seconds  
(without alignments)  
6916.451 Million cell updates/sec

Title: US-10-032-254A-1  
Perfect score: 1554  
Sequence: 1 gttgcggagtcctccactc.....caaaaaaaaaaaaaaaaaaaaaa 1554

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_htg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID         | Description        |
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| 2          | 1456   | 93.7        | 1498   | 10 BC051996   | BC051996 Mus muscu |
| 3          | 1454.4 | 93.6        | 1489   | 10 BC055891   | BC055891 Mus muscu |
| 4          | 1340.4 | 86.3        | 1618   | 10 AB004267   | AB004267 Rattus no |
| 5          | 1261.2 | 81.2        | 1458   | 6 AR411048    | AR411048 Sequence  |
| 6          | 1032   | 66.4        | 1032   | 10 AB023027   | AB023027 Mus muscu |
| 7          | 979.2  | 63.0        | 1332   | 10 D86556     | D86556 Rattus norv |
| 8          | 844.4  | 54.3        | 1282   | 6 AR139102    | AR139102 Sequence  |
| 9          | 844.4  | 54.3        | 1282   | 6 AR270390    | AR270390 Sequence  |
| 10         | 836.8  | 53.8        | 1032   | 6 AX165520    | AX165520 Sequence  |
| 11         | 809    | 52.1        | 1624   | 9 BC064422    | BC064422 Homo sapi |
| 12         | 781.6  | 50.3        | 964    | 6 CQ728144    | CQ728144 Sequence  |
| 13         | 534.4  | 34.4        | 2831   | 5 AB098710    | AB098710 Xenopus l |
| 14         | 512    | 32.9        | 1439   | 10 RATCAMPKAA | L26288 Rattus norv |
| 15         | 512    | 32.9        | 1445   | 10 BC071177   | BC071177 Rattus no |
| 16         | 510.4  | 32.8        | 1448   | 10 BC014825   | BC014825 Mus muscu |
| 17         | 502.4  | 32.3        | 1402   | 10 RATERKI    | L24907 Rattus norv |
| 18         | 500.8  | 32.2        | 1113   | 12 AY335764   | AY335764 Synthetic |
| 19         | 500.8  | 32.2        | 1480   | 6 AR270891    | AR270891 Sequence  |

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| 21 | 500.8 | 32.2 | 1480 | 9  | HUMCKI    | L41816 Homo sapien |
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| 23 | 454.4 | 29.2 | 1149 | 5  | AB083000  | AB083000 Xenopus l |
| 24 | 450.4 | 29.0 | 1506 | 5  | CR761672  | CR761672 Xenopus t |
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| 26 | 436.2 | 28.1 | 1074 | 6  | AR373295  | AR373295 Sequence  |
| 27 | 436.2 | 28.1 | 1074 | 6  | AX166517  | AX166517 Sequence  |
| 28 | 436.2 | 28.1 | 1074 | 6  | AX167587  | AX167587 Sequence  |
| 29 | 436.2 | 28.1 | 1158 | 6  | AR373294  | AR373294 Sequence  |
| 30 | 436.2 | 28.1 | 1158 | 6  | AX167585  | AX167585 Sequence  |
| 31 | 436.2 | 28.1 | 1579 | 6  | CQ776505  | CQ776505 Sequence  |
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| 33 | 436.2 | 28.1 | 1661 | 6  | AX680144  | AX680144 Sequence  |
| 34 | 436.2 | 28.1 | 1671 | 6  | AR373296  | AR373296 Sequence  |
| 35 | 436.2 | 28.1 | 1671 | 6  | AX167589  | AX167589 Sequence  |
| 36 | 436.2 | 28.1 | 1733 | 6  | AR339035  | AR339035 Sequence  |
| 37 | 436.2 | 28.1 | 1736 | 6  | AX680135  | AX680135 Sequence  |
| 38 | 436.2 | 28.1 | 1800 | 9  | BC035745  | BC035745 Homo sapi |
| 39 | 436.2 | 28.1 | 2235 | 9  | AB081726  | AB081726 Homo sapi |
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## ALIGNMENTS

RESULT 1  
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LOCUS AF181984 1554 bp mRNA linear ROD 22-FEB-2000  
DEFINITION Mus musculus pregnancy upregulated nonubiquitous  
Ca2+/calmodulin-dependent kinase Pnck mRNA, complete cds.

ACCESSION AF181984

VERSION AF181984.1 GI:6841607

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 1554)

AUTHORS Gardner,H.P., Rajan,J.V., Ha,S.I., Copeland,N.G., Gilbert,D.J.,

Jenkins,N.A., Marquis,S.T. and Chodosh,L.A.

TITLE Cloning, characterization, and chromosomal localization of Pnck, a

Ca(2+)/calmodulin-dependent protein kinase

JOURNAL Genomics 63 (2), 279-288 (2000)

MEDLINE 20139438

PUBMED 10673339

REFERENCE 2 (bases 1 to 1554)

AUTHORS Gardner,H.P. and Chodosh,L.A.

TITLE Direct Submission

JOURNAL Submitted (31-AUG-1999) Molecular and Cellular Engineering,

University of Pennsylvania, 612 BRBII/III, 421 Curie Blvd,

Philadelphia, PA 19104-6160, USA

FEATURES

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## ORIGIN

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## RESULT 2

BC051996

LOCUS

DEFINITION

Mus musculus pregnancy upregulated non-ubiquitously expressed Cam

kinase, mRNA (cdna clone IMAGE:5693661), partial cds.

ACCESSION

BC051996

VERSION

BC051996.1

KEYWORDS

Mus musculus (house mouse)

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 1498)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klauser, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raja, S.S., Loquellano, N.A., McEwan, P.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahney, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

TITLE Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL MEDLINE  
PUBMED 22388257  
REFERENCE 12477932  
2 (bases 1 to 1498)  
Strausberg, R.  
Direct Submission  
Submitted (01-MAY-2003) National Institutes of Health, Mammalian  
Gene Collection (MGC) Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
COMMENT Contact: MGC help desk  
Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)  
Tissue Procurement: Dr. Jim Lin, University of Iowa  
cDNA Library Preparation: M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (fLNL)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome  
Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www-shgc.stanford.edu>  
Contact: (Dickson, Mark) [med@paxil.stanford.edu](mailto:med@paxil.stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
R. M.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/fLNL at: <http://image.llnl.gov>  
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## ORIGIN

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VERSION BC055891.1 GI:33585934
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1489)
AUTHORS Strausberg R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
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Bouffard, G.C., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smal, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
REFERENCE 2 (bases 1 to 1489)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
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Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www-shgc.stanford.edu>  
Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAK Plate: 120 Row: j Column: 1  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6753247.

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ACCESSION AR411048
VERSION AR411048.1 GI:40162652
KEYWORDS
SOURCE Unknown.
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REFERENCE 1 (bases 1 to 1458)
AUTHORS Sutcliffe,J.G., Gautvik,K.M., De Lecea,L., Bloom,F.E.,
Danielson,P.E., Gautvik,V.T., Kilduff,T.S. and Foye,P.E.
TITLE Hypothalamic-specific polypeptides
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SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

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AUTHORS Ueda,T. and Minami,Y.
TITLE mCamK1-beta2
JOURNAL Published Only in DataBase (1999)
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AUTHORS Ueda,T. and Minami,Y.
TITLE Direct Submission
JOURNAL Submitted (29-JAN-1999) Takahiro Ueda, Kobe University School of
Medicine, Dep of Biochemistry; 7-5-1, Kusunoki-Cho, Chuo-Ku, Hyogo
650-0017, Japan (E-mail:ueda@med.kobe-u.ac.jp,
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LOCUS D86556 1332 bp mRNA linear ROD 07-FEB-1999
DEFINITION Rattus norvegicus mRNA for Protein Kinase, complete cds.
ACCESSION D86556
VERSION D86556.1 GI:2077931
KEYWORDS Protein Kinase.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
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          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus.
          1 (bases 1 to 1332)
          Yokokura,H., Terada,O., Naito,Y. and Hidaka,H.
          Isolation and comparison of rat cDNAs encoding
          Ca2+/calmodulin-dependent protein kinase I isoforms
          Biochim. Biophys. Acta 1338 (1), 8-12 (1997)
          9074610
          PUBMED 97228532
          2 (bases 1 to 1332)
          Yokokura,H.
          Direct Submission
          TITLE
```

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JOURNAL Submitted (15-JUL-1996) Hisayuki Yokokura, Nagoya University School
of Medicine, Department of Pharmacology, Tsurumai 65, Showa-ku,
Nagoya, Aichi 466, Japan (tel:052-744-2075, Fax:052-744-2083)
FEATURES
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DEFINITION Sequence 953 from patent US 6500938.  
ACCESSION AR270390  
VERSION AR270390.1 GI:29701624  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1282)  
AUTHORS Au-Young, J. and Seilhamer, J.J.  
TITLE Composition for the detection of signaling pathway gene expression  
JOURNAL Patent: US 6500938-A 953 31-DEC-2002;  
FEATURES Location/Qualifiers  
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LOCUS AX166520 1032 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 11 from Patent WO0138503.  
ACCESSION AX166520  
VERSION AX166520.1 GI:14546865  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Plowman, G.D., Whyte, D., Manning, G.S., Sudarsanam, S.S., Martinez, R.,  
Flanagan, P. and Clary, D.S.  
TITLE Novel human protein kinases and protein kinase-like enzymes  
JOURNAL Patent: WO 0138503-A 11 31-MAY-2001;  
Sugen, Inc. (US)  
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VERSION  
KEYWORDS  
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REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REMARK  
COMMENT  
FEATURES  
source

BC064422 1624 bp mRNA linear PRI 06-JUL-2004  
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kinase, mRNA (cDNA clone MGC:70892 IMAGE:5751849), complete cds.  
BC064422  
BC064422.1 GI:39962914  
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1 (bases 1 to 1624)  
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,  
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,  
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,  
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Haieh,F.,  
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Sapleton,M., Brownstein,M.J., Ustin,T.B., Loquellano,N.A., Peters,G.J.,  
Carninci,P., Prange,C., Raha,S.S., Lodigiano,N.A., McEwan,P.J.,  
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McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,  
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,  
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,  
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,  
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,  
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,  
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,  
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalius,D.E.,  
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
2 (bases 1 to 1624)  
Strausberg,R.  
Direct Submission  
Submitted (15-DEC-2003) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC),  
Gaithersburg, Maryland:  
Web site: <http://www.nisc.nih.gov/>  
Contact: [nisc\\_mgc@hgr.nih.gov](mailto:nisc_mgc@hgr.nih.gov)  
Akhtar,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,  
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,  
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,  
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,  
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,  
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,  
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,  
Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAC Plate: 139 Row: m Column: 20  
This clone was selected for full length sequencing because it  
passed the following selection criteria: Similarity but not  
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Query Match 52.1%; Score 809; DB 9; Length 1624;
Best Local Similarity 74.1%; Pred. No. 1.8e-201; Mismatches 275; Indels 134; Gaps 6;
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CQ728144
CQ728144.1 GI:42296190
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
AUTHORS
  Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE
  Kits, such as nucleic acid arrays, comprising a majority of
  humanexons or transcripts, for detecting expression and other uses
  thereof
JOURNAL
  Patent: WO 02068579-A 14078 06-SEP-2002;
  PE Corporation (NY) (US)
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ACCESSION
  AB098710
VERSION
  AB098710.1 GI:32261077
KEYWORDS
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ORGANISM
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REFERENCE
  1 Kinoshita, S., Sueyoshi, N., Tsuge, T., Suetake, I., Tajima, S. and
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  Molecular cloning and expression of X. laevis CaMKI-like protein
  Unpublished
  2 (bases 1 to 2831)
  Kameshita, I., Kinoshita, S., Sueyoshi, N., Tsuge, T., Suetake, I. and
  Tajima, S.
  Direct Submission
  Submitted (25-DEC-2002) Isamu Kameshita, Kagawa University,
  Department of Life Sciences, 2393, Ikenobe, Miki-cho, Kita-gun,
  Kagawa 761-0795, Japan (E-mail:kamesita@ag.kagawa-u.ac.jp,
  Tel:81-87-891-3120, Fax:81-87-891-3120)
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LOCUS Rattus norvegicus Cam-like protein kinase mRNA, complete cds.  
DEFINITION L26288  
ACCESSION L26288  
VERSION 1  
KEYWORDS protein kinase.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE 1 (bases 1 to 1439)  
AUTHORS Cho, F.S., Phillips, K.S., Bogucki, B. and Weaver, T.E.

TITLE Characterization of a rat cDNA clone encoding  
JOURNAL calcium/calmodulin-dependent protein kinase I  
MEDLINE Biochim. Biophys. Acta 1224 (1), 156-160 (1994)  
PUBMED 95035115  
COMMENT 7948038  
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| JOURNAL    |      |   |      |
| PUBMED     |      |   |      |
| REFERENCE  |      |   |      |
| AUTHORS    |      |   |      |
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| QY                    | 239 | CATTCCCAAGAAAGCACTTCGGGGCAAGGAGCCCTGGTGGAGAAATGAGATCGCGGTACT  | 298   |
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| QY                    | 299 | TCCAGAAATCAGCCATCCCAACATTTGTGGCTCTTGGAGGAGCTGCATGAGATGCTTCTCA | 358   |
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| Query Match           |     | 32.9%   | Score 512; DB 10; Length 1445;                    |
| Best Local Similarity |     | 72.7%   | Pred. No. 2.4e-123;                               |
| Matches               |     | 675;  | Conservative 0; Mismatches 250; Indels 3; Gaps 1; |

CDNA Library Preparation: Express Genomics  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
 DNA Sequencing by: National Institutes of Health Intramural  
 Sequencing Center (NISC),  
 Gaithersburg, Maryland;  
 web site: <http://www.nisc.nih.gov/>  
 Contact: nisc\_mgc@nih.gov  
 Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,  
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 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
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 /db\_xref="RGD:629473"  
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 YENDAKLFEQILKAEYEFDSPYWDDIISAKDFIRHLMKDFEKFCTCQALQHPWI  
 AGDTALDKNIHOSVBIKKNFAKSKWQAFNATAVVRHMRKLQLGTSQEGQGTASH  
 GELLTPTAGGPAAGCCCRDCCVPGSELPPPPSSRAMD"





GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 5, 2005, 22:38:35 ; Search time 1266 Seconds  
(without alignments)  
7266.412 Million cell updates/sec

Title: US-10-032-254A-1  
Perfect score: 1554  
Sequence: 1 gttcggagtcctccactc.....caaaaaaaaaaaaaaaaaa 1554

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16Dec04.\*

1: Geneseqn1980s.\*  
2: Geneseqn1990s.\*  
3: Geneseqn2000s.\*  
4: Geneseqn2001as.\*  
5: Geneseqn2001bs.\*  
6: Geneseqn2002as.\*  
7: Geneseqn2002bs.\*  
8: Geneseqn2003as.\*  
9: Geneseqn2003bs.\*  
10: Geneseqn2003cs.\*  
11: Geneseqn2003ds.\*  
12: Geneseqn2004as.\*  
13: Geneseqn2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | ID          | Description         |
|------------|--------|-------------|--------|-------------|---------------------|
| 1          | 1261.2 | 81.2        | 1458   | 2 AAV18867  | AAV18867 Calmoduli  |
| 2          | 859    | 55.3        | 1584   | 12 ADM43841 | Adm43841 Novel hum  |
| 3          | 844.4  | 54.3        | 1282   | 2 AAX06835  | Aax06835 Disease a  |
| 4          | 844.4  | 54.3        | 1282   | 10 ACA56355 | Acas56355 Norway ra |
| 5          | 844.4  | 54.3        | 1282   | 12 ADI56151 | Adi56151 Human pol  |
| 6          | 844.4  | 54.3        | 1282   | 12 ADL06429 | Adl06429 Human tum  |
| 7          | 844.4  | 54.3        | 1282   | 12 ADM72654 | Adm72654 Human TAS  |
| 8          | 844.4  | 54.3        | 1282   | 12 ADM72236 | Adm72236 Human TAS  |
| 9          | 836.8  | 53.8        | 1032   | 4 AAS06711  | Aas06711 Polynucle  |
| 10         | 803.6  | 51.7        | 1216   | 6 ABZ11323  | Abz11323 Human pol  |
| 11         | 800.2  | 51.5        | 1180   | 13 ADR39798 | Adr39798 Human kin  |
| 12         | 699    | 45.0        | 1656   | 8 ACC46211  | Acc46211 Human dit  |
| 13         | 681.8  | 43.9        | 1371   | 8 ACC46241  | Acc46241 Human dit  |
| 14         | 671.6  | 43.2        | 1646   | 12 ADE28342 | Ades28342 Human Kpp |
| 15         | 588.8  | 37.9        | 1120   | 12 ADI40898 | Adi40898 Human kin  |
| 16         | 544    | 35.0        | 641    | 12 ADM72664 | Adm72664 Human TAS  |
| 17         | 512    | 32.9        | 1439   | 10 ADB53683 | Adb53683 Primary r  |
| 18         | 502.4  | 32.3        | 1402   | 10 ADB57940 | Adb57940 Toxicity   |
| 19         | 500.8  | 32.2        | 1480   | 8 RAD52784  | Rad52784 Human cam  |
| 20         | 500.8  | 32.2        | 1480   | 10 ACA56856 | Acas56856 Human sig |

|    |       |      |      |             |                    |
|----|-------|------|------|-------------|--------------------|
| 21 | 500.8 | 32.2 | 1480 | 12 ADI56652 | Adi56652 Human pol |
| 22 | 500.8 | 32.2 | 1501 | 12 ADL97819 | Adl97819 Human typ |
| 23 | 500.8 | 32.2 | 1501 | 13 ADP23703 | Adp23703 PRO polyp |
| 24 | 447.6 | 28.8 | 1197 | 12 ADI40938 | Adi40938 Human kin |
| 25 | 437.8 | 28.2 | 1736 | 4 AAI18817  | Aai18817 Human kin |
| 26 | 436.2 | 28.1 | 1074 | 4 AAS06708  | Aas06708 Polynucle |
| 27 | 436.2 | 28.1 | 1074 | 4 AAH25119  | Aah25119 Nucleotid |
| 28 | 436.2 | 28.1 | 1158 | 4 AAH25118  | Aah25118 Nucleotid |
| 29 | 436.2 | 28.1 | 1565 | 6 ABL60905  | AbL60905 Human Cam |
| 30 | 436.2 | 28.1 | 1578 | 4 AAD04775  | Aad04775 Human dea |
| 31 | 436.2 | 28.1 | 1579 | 12 ADJ74939 | Adj74939 Marker ge |
| 32 | 436.2 | 28.1 | 1579 | 12 ADQ15043 | Adq15043 Human can |
| 33 | 436.2 | 28.1 | 1661 | 4 AAD18826  | Aad18826 Human kin |
| 34 | 436.2 | 28.1 | 1671 | 4 AAH25120  | Aah25120 Nucleotid |
| 35 | 436.2 | 28.1 | 1733 | 4 AAI58638  | Aai58638 Human pol |
| 36 | 436.2 | 28.1 | 1733 | 5 ADO98856  | Ado98856 DNA encod |
| 37 | 436.2 | 28.1 | 1733 | 9 ADB48616  | Adb48616 Novel hum |
| 38 | 436.2 | 28.1 | 2164 | 4 AAI60424  | Aai60424 Human pol |
| 39 | 431.2 | 27.7 | 709  | 4 ABK43538  | Abk43538 DNA encod |
| 40 | 431.2 | 27.7 | 709  | 12 ADI53925 | Adi53925 cDNA enco |
| 41 | 430   | 27.7 | 1383 | 6 ABK99973  | Abk99973 Human CAD |
| 42 | 430   | 27.7 | 1738 | 6 ABK99974  | Abk99974 Human CAD |
| 43 | 430   | 27.7 | 1956 | 4 AAI60703  | Aai60703 Human pol |
| 44 | 428.4 | 27.6 | 2447 | 6 AAD36140  | Aad36140 Human cal |
| 45 | 428.2 | 27.6 | 1694 | 4 AAC90432  | Aac90432 Murine de |

## ALIGNMENTS

## RESULT 1

AAV18867  
ID AAV18867 standard; cDNA; 1458 BP.

AC AAV18867;

XX 09-JUL-1998 (first entry)

XX Calmodulin-dependent protein kinase clone 29 cDNA.

XX Rat; calmodulin-dependent protein kinase; clone 29; ds.

XX Rattus rattus.

XX Key Location/Qualifiers

FT CDS 50..1125

FT /\*tag= a

FT /product= "calmodulin-dependent protein kinase"

FT /transl\_except= (pos:1079..1080, aa:Val)

FT /note= "this codon has an apparent 1 nucleotide deletion, that alters the reading frame"

XX W09805352-A1.

XX 12-FEB-1998.

XX 01-AUG-1997; 97WO-US013657.

XX 02-AUG-1996; 96US-0023220P.

XX (SCRI ) SCRIPPS RES INST.

XX Sutcliffe JG, Gautvik KM, De Lecea L, Bloom FE, Danielson PE;

XX Gautvik VT, Kilduff IS, Foye PE;

XX WPI; 1998-145352/13.

XX P-PSDB; AAW50159.

XX Nucleic acid encoding hypocretin of rat and mouse - useful for diagnosis and treatment of neurological disease, homeostatic dysfunction etc., also sequence for calmodulin kinase-like protein.

XX Claim 55; Fig 6; 111pp; English.

|    |   |  |
|----|---|--|
| XX | CC  | The present sequence encodes rat calmodulin-dependent protein kinase |
| CC | clone 29  |  |
| XX | XX  |  |
| SQ | Sequence 1458 BP; 311 A; 406 C; 403 G; 338 T; 0 U; 0 Other; |  |
|    | Query Match   | 81.2%; Score 1261.2; DB 2; Length 1458;                              |
|    | Best Local Similarity                                       | 93.6%; Pred. No. 0;  |
|    | Matches 1348; Conservative                                  | 0; Mismatches 63; Indels 29; Gaps 2;                                 |
| QY | 99  | GCAGACATGCTGCTCTCAAGAAACACAGCGAGGACATCAGCACTGCTCTATGAGATCCGG 158     |
| DB | 44  | GCAGACATGCTGCTCTCAAGAAACACAGCGAGGACATCAGCACTGCTCTATGAGATCCGG 103     |
| QY | 159   | GAGAAGCTGGGCTGGGTGCTTCTCTGAGGTGATGTGGCCACAGGAAAGGGGCTCTGCT 218       |
| DB | 104   | GAGAAGCTGGGCTGGGTGCTTCTCTGAGGTGATGTGGCCACAGGAAAGGGGCTCTGCT 163       |
| QY | 219   | CATCTTCTGGCCCTCAAGTGCATTTCCCAAGAAAGCACTTCGGGCAAGGAGGCCCTGGTG 278     |
| DB | 164   | CATCTTGTGGCCCTCAAGTGCATTTCCCAAGAAAGCACTTCGGGCAAGGAGGCCCTGGTG 223     |
| QY | 279   | GAGAATGAGATCGCGGTACTTCGCAGAAATCAGCCATCCCAACATTTGGCTCTGGAGGAC 338     |
| DB | 224   | GAGAATGAGATCGCAGTACTCCGACGATTAGCCACCCCAACATTTGGCTCTGGAGGAC 283       |
| QY | 339   | GTCCATCAGAGTCCCTCTCATCTCTACTTGGCCATGAGCTGCTTAACAGTGTGTGACTG 398      |
| DB | 284   | GTCCACAGAGCCCTTCCCATCTCTACTTGGCCATGAGCTGCTTAACAGTGTGTGAACTG 343      |
| QY | 399   | TTTGACCGCATCATGGAGCGGGCTCCCTACACAGAGAAGGACGCCACCCACCTTGTAGGG 458     |
| DB | 344   | TTTGACCGAATCATGGAGCGGGCTCCTACACAGAGAAGGATCGAGCCACCTTGTAGGG 403       |
| QY | 459   | CAGTCTTGGCGTGTCTCTCTACTCTATAGCCTTGGGCAATCGTGTCAACGGGACCTCAAG 518     |
| DB | 404   | CAGTCTTGGTGTGTCTCTCTACTCTATAGCCTTGGGCAATCGTGTCAACGGGACCTCAAG 463     |
| QY | 519   | CCTGAAACCTCTCTATGCGACACCTTTTGGAGACTCCAAGATCATGGTCTCTGACTTT 578       |
| DB | 464   | CCTGAAACCTCTCTATGCGACACCTTTTGGAGACTCCAAGATCATGGTCTCTGACTTT 523       |
| QY | 579   | GGCCTGTCCAAATACAAGCTGGCAACATGCTAGGCAAGCTGTGGGACCCCGAGGATAT 638       |
| DB | 524   | GGCCTGTCCAAATTTCAAGCTGGCAACATGCTAGGCAAGCTGTGGGACCCCGAGGATAT 583      |
| QY | 639   | GTGGCCCGAGCTCTCTGGAGCAAAACCTTACGGGAGGCCGTAGATGTGTGGGCCCTG 698        |
| DB | 584   | GTGGCCCGAGAGTCTCTGGAGCAAAACCTTACGGGAGGCCGTAGATGTGTGGGCCCTG 643       |
| QY | 699   | GGTGTCTATCTCTACATCTCTGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCT 758        |
| DB | 644   | GGTGTCTATCTCTACATCTCTGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCT 703        |
| QY | 759   | GAACTTTACGCCAGATTCTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGAC 818      |
| DB | 704   | GAACTTTACGCCAGATTCTGAGGGCCAGCTATGAGTTTGACTCTCCCTTTTGGGATGAC 763      |
| QY | 819   | ATCTCAGAAATCAGCAAGAGCTTCAATTCGCCACCTTCTGGAAACGTGATCCCCAGAAAGG 878    |
| DB | 764   | ATCTCAGAAATCAGCCAAAGACTTCAATTCGGGACCTTCTGGAAACGTGATCCCCAGAAAGG 823   |
| QY | 879   | TTACCTTCCAGCGAGGCCCTACAGCATTTTGGATCTCTGGGATGAGCGCTTCGATAGG 938       |
| DB | 824   | TTACCTTCCCAACAGGCCCTTACAGCATCTCTGTGATCTCTGGGATGAGCGCTTGGACAGG 883    |
| QY | 939   | GACATCTGGGTCTGTCTCAGTGAGCAGATCCAGAGAAATTTTGCCAGGACCCACTGGAAG 998     |
| DB | 884   | GACATCTTAGTCTCTGTCTCAGTGAGCAGATCCAGAGAAATTTTGCCAGGACCCACTGGAAG 943   |
| QY | 999   | CGTGCAATTCATGCCCACATCAATCTCTACGTCCATCCGTATAGCTGGGACAAAGCCCAGAG 1058  |
| DB | 944   | CGTGCAATTCATGCCCACATCAATCTCTACGTCCATCCGTATAGCTGGGACAAAGCCCAGAG 1003  |

The invention relates to an isolated polynucleotide. The methods and compositions of the present invention are useful for the diagnosis and/or treatment of diseases or conditions associated with aberrant expression or activity of the arginine-rich protein-like polypeptides, such as cancer and inflammation. They can also be used in forensics, gene mapping, identification of mutations responsible for genetic disorders, and in assessing biodiversity. The present sequence represents a novel human arginine-rich protein cDNA.

Sequence 1584 BP; 282 A; 530 C; 457 G; 315 T; 0 U; 0 Other;

Query Match 55.3%; Score 859; DB 12; Length 1584;

Best Local Similarity 78.7%; Pred. No. 4.3e-216;

|  |
|--|
| Matches 1098; Conservative 0; Mismatches 270; Indels 27; Gaps 5; |
|--|

|    |      |   |      |
|----|------|---|------|
| Qy | 168  | GGCTCGGGTGCCTTCTCTGAGGTGATGCTGTGCCACGAGAAAGGGGCTCTGCTCATCTTTGTG | 227  |
| Db | 201  | GGCAGGGGTGCCCTTCTCCGAGGTGTGCTGTGCCACGAGCGGGGCTCCGACACCTCGTG     | 260  |
| Qy | 228  | GCCTCAAGTGCATTCCCAAGAAAGACACTTCGGGGCAAGGAGGCCCTGTGTGGAGAAATGAG  | 287  |
| Db | 261  | GCCTCAAGTGCATCCCAAGNAGGCCCTCGGGGCAAGNAGGCCCTGTGTGGAGAACGAG      | 320  |
| Qy | 288  | ATCGCGGTACTTTCGAGAAATCAGCCATCCCAAACAATGTGTGCTGTGGAGGACGTCCATGAG | 347  |
| Db | 321  | ATCGCAGTGTCCGTAGGATCAGTCACCCCAAACATCGTCTCTGGAGGATGTCCAGGAG      | 380  |
| Qy | 348  | AGTCTCTTCATCTCTACTTGGCCATGGAGCTGTGTACAGGTGTGTGAACCTGTGTGTGACCGC | 407  |
| Db | 381  | AGCCCTTCCCACTCTACTTGGCCATGGAACTGTGTGACGGGTGGGAGCTGTGTGTGACCGC   | 440  |
| Qy | 408  | ATCATGGAGCGGGCTCCTACAGAGAAGAACGCCAGCCACCTTGTAGGGCAGGTCTCTT      | 467  |
| Db | 441  | ATCATGGAGCGGGCTCCTACAGAGAAGATGSCAGACCATCTGTGTGGTTCAGGTCTCTT     | 500  |
| Qy | 468  | GGCGCTGTCTCTACCTTTCATAGCTTGGGCATCGTGCAACGGGACCTCAAGCCTGAAAAAC   | 527  |
| Db | 501  | GGCGCGCTGTCTCTACCTGTCAAGCCTTGGGATCGTGCAACGGGACCTCAAGCCTGAAAAAC  | 560  |
| Qy | 528  | CTCCTCTATGCCACACCTTTTGGAGACTCCAAAGATCATGTCTCTGACTTTTGGCTCTGCC   | 587  |
| Db | 561  | CTCCTGTATGCCACGCCCTTTGAGGACTCGAAGATCATGTCTCTGACTTTGACTCTCC      | 620  |
| Qy | 588  | AAAATCAAGCTGGCAACATGCTAGGCACAGCCTGTGGGACCCACAGGATATGTGGCCCCA    | 647  |
| Db | 621  | AAAATCAGGCTGGGAACATGCTAGGCACAGCCTGTGGGACCCCTGATATGTGGCCCCA      | 680  |
| Qy | 648  | GAGCTCTGAGCAGAAACCTTACGGGAAGGCGTAGATGTGTGGGCCCTGGGTGTCATC       | 707  |
| Db | 681  | GAGCTCTTGGAGCAGAAACCTTACGGGAAGGCGTAGATGTGTGGGCCCTGGGGGTGTCATC   | 740  |
| Qy | 708  | TCCTTACATCTGTGTGTGGGTACCCGCCCTTCTATGATGAGACGATCTCTGAATCTTTC     | 767  |
| Db | 741  | TCCTTACATCTGTGTGTGGGTACCCGCCCTTCTACGACGAGACGACCTTGAGCTCTTC      | 800  |
| Qy | 768  | AGCCAGATTCTGAGGGCCAGCTATGAGTTTGAATCTCCGCCCTTTTGGGATGATCATCTAGAA | 827  |
| Db | 801  | AGCCAGATCTGAGGGCCAGCTATGAGTTTGAATCTCTCTTCTTGGGATGATCATCTAGAA    | 860  |
| Qy | 828  | TCAGCCAAAAGACTTCATTTCGCCACTTCTTGAACTGATCCCCAAGAGAGGTTTCACTGTC   | 887  |
| Db | 861  | TCAGCCAAAAGACTTCATTTCGCCACTTCTTGAGGCGAGACCCCAAGAGAGGTTTCACTGTC  | 920  |
| Qy | 888  | CAGCAGGCCCTTACAGCATCTTTGGATCTCTGGGGATCAGCCTTTCGATAGGGACATCTTG   | 947  |
| Db | 921  | CAACAGGCCCTTTCGCCACTTGGATCTCTGGGGACACAGCCTTTCGACAGGACATCTTA     | 980  |
| Qy | 948  | GGTCTCTGCTAGTGACAGATCCAGAAATTTTGCAGGACCCACTCGAGGCGTGCATTC       | 1007 |
| Db | 981  | GGCTCTCTGCTAGTGACAGATCCGGAAGAACTTTGCTCGGACACACTCTGGAAGCGAGCTTC  | 1040 |
| Qy | 1008 | AATGCCACATCATTTCTTCAGTTCATCCGTAACTGGGACAAAAGCCACAGAGGTGAGGAG    | 1067 |

|  |  |  |   |   |   |                                  |   |  |  |  |
|--|--|--|---|---|---|----------------------------------|---|--|--|--|
|  |  | 19-JUN-1997; 97US-00878989.<br>(INCY-) INCYTE PHARM INC. | Bandman O, Hillman JL, Corley NC, Guegler KJ, Lal P, Golli SK;<br>Shah P; | WPI; 1999-080952/07.<br>P-PSDB; AAW88436. | New disease associated protein kinases - used to stimulate cell<br>proliferation and to treat the immune response and cancer. | Claim 5; Page 65; 93pp; English. | This cDNA sequence codes for human disease associated protein kinase DAPK<br>-5 (see AAW88436). DAPK-5 cDNA was first identified in the PROSNOT06 CDNA<br>library using a computer search for amino acid alignments, and a<br>consensus sequence was derived from the extended and overlapping Incyte<br>clones 75501, 758002 and 760552/BRAITUT02, 827431/PROSNOT06.<br>1286067/COLANNOR16 and 1503272/BRAITUT07. DAPK-5 shows 64% homology with<br>the human CAM-Kinase CAMKI (GI 790790), and is associated with CDNA<br>libraries which are immortalised or cancerous. The invention provides<br>DAPK-1 to DAPK-7 proteins (see AAW88432-38) and CDNA clones encoding them<br>(see AAX06831-36 and AAX06882), as well as expression vectors, host<br>cells, agonists, antagonists and antibodies. The invention further<br>provides uses of such products in the diagnosis, prevention and treatment<br>of diseases associated with cell proliferation, especially cancer or an<br>immune response (claimed). Conditions that may be treated include adult<br>respiratory distress syndrome, allergies, asthma, arteriosclerosis,<br>bronchitis, emphysema, hyper eosinophilia, myocardial or pericardial<br>inflammation, rheumatoid arthritis, Addison's disease, AIDS, anaemia,<br>atherosclerosis, various diseases of the digestive system, atopic<br>dermatitis, dermatomyositis, diabetes mellitus, glomerulonephritis, gout,<br>Grave's disease, lupus erythematosus, multiple sclerosis, myasthenia<br>gravis, osteoarthritis, osteoporosis, pancreatitis, polycystic kidney<br>disease, polymyositis, scleroderma, Sjogren's syndrome, autoimmune<br>thyroiditis, complications of cancer, extracorporeal circulation, viral,<br>bacterial, fungal, parasitic, protozoal and helminthic infections, and<br>CC trauma (disclosed). The DAPK nucleic acids are also used in a method for<br>XX detection of DAPK expression levels in a biological sample | SQ Sequence 1282 BP; 275 A; 370 C; 383 G; 245 T; 0 U; 9 Other; | Query Match 54.3%; Score 844.4; DB 2; Length 1282;<br>Best Local Similarity 86.2%; Pred. No. 2.8e-212;<br>Matches 940; Conservative 1; Mismatches 145; Indels 4; Gaps 1; | 101 AGACATGCTCCTCAAGAAACAGACGAGGACATCACAGTGTTCATGAGATCCGGGA 160<br>197 AACATCTCTCTGAAGAANAACACGAGGAGCATCACAGCGTCTAGAGATCCGGGA 256<br><br>161 GAAGCTGGGCTCGGGTGCCCTTTCTGAGGTGTATGCTGGGCCAAGGAAGGGCTCTGTCTCA 220<br>257 GAGGCTCGGCTCGGTGCCTTCTCCGAGGTGTGTCTGGGCCAAGGCGGGCTCCGCACA 316<br><br>221 TCATTGTGGCCCTCAAAGTGACATCCCAGAAGAACACTTTCGGGGCAAGAGGCCCTGGTGA 280<br>317 CCTCGTGGCCCTCAAAGTGACATCCCCAAGAAGGCCCTCCGGGGCAAGAGGCCCTGGTGA 376<br><br>281 GAATGAGATCCGGTACTTCGGAGATCATGCCATCCACATGTGGCTCTGGAGAGCT 340<br>377 GAACGAGATCCGAGTGTCTCGTAGGATCAAGTACCACCAACATCGTGTCTGGAGGATGT 436<br><br>341 CCATGAGGTCTCTCATCTCTACTTGGCCATGGAGCTGGTAACAGAGGTGGTGAAGCTGTT 400<br>437 CCACGAGAGCCCTTCCCACCTCTACCTGGCCATGGAACTGGTGAACGGTGGGAGCTGTT 496<br><br>401 TGACCGCATCATGGAGCGGGCTCTCTACACAGAGAAGAGCGCCAGCCACTTGTAGGGCA 460<br>497 TGACCGCATCATGGAGCGGGCTCTCTACACAGAGAAGAGTGGCAGCCATCTGGTGGGTCA 556 |
|--|--|--|---|---|---|----------------------------------|---|--|--|--|



```
PF 26-NOV-2002; 2002US-00305720.
XX
PR 30-JAN-1998; 98US-00016434.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Au-Young J, Seilhamer JJ;
XX WPI; 2004-090520/09.
XX
DR New composition comprising polynucleotide probes, useful as array
PT elements in a microarray for monitoring the expression of target
PT polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic
PT fragments.
XX
PS Claim 6; SEQ ID NO 953; 73pp; English.
XX
CC The invention relates to a composition of polynucleotide probes
CC comprising first polynucleotide probes comprising at least a portion of a
CC gene encoding a receptor-like polypeptide, second polynucleotide probes
CC comprising at least a portion of a gene encoding a transducing
CC polypeptide and third polynucleotide probes comprising at least a portion
CC of a gene encoding an effector-like polypeptide. The probes of the
CC composition are useful as array elements in a microarray for monitoring
CC the expression of target polynucleotides. The microarray is useful in the
CC diagnosis and treatment of cancer, an immunopathology or a
CC neuropathology. It can also be used for drug discovery and development,
CC toxicological and carcinogenicity studies, forensics or pharmacogenomics.
CC Microarrays can also be used for monitoring the progression of diseases
CC that may be associated with the altered expression of signalling pathway
CC polypeptides. The composition can also be used to purify a subpopulation
CC of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile
CC is also useful for the diagnosis and treatment of cancer, e.g. cancers of
CC the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix,
CC an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or
CC ulcerative colitis, or a neuropathology, e.g. dementia, amnesia,
CC epilepsy, Alzheimer's disease or depression. This sequence represents a
CC human polynucleotide probe of the invention. Note: the sequence data for
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 1282 BP; 275 A; 370 C; 383 G; 245 T; 0 U; 9 Other;

Query Match 54.3%; Score 844.4; DB 12; Length 1282;
Best Local Similarity 86.2%; Pred. No. 2.8e-212;
Matches 940; Conservative 1; Mismatches 145; Indels 4; Gaps 1;

QY 101 AGACATGCTGCTCAAGAACAGACGAGGAGCATCAGCAGTGCTCTATGAGATCCGGGA 160
DB 197 AAACATGCTGCTGCTGAAGAAACACACGAGGAGCATCAGCAGTGCTCTACGAGATCCGCGA 256

QY 161 GAAGCTGGGTGCGGTGCTTCTCTGAGGTGATGCTGGCCAGGAAAGGGGCTCTGCTCA 220
DB 257 GAGGCTGGGTGCGGTGCTTCTCCGAGGTGGTGTGCTGGCCAGGAGCGGGGCTCCGCACA 316

QY 221 TCTTGTGGCCCTCAAGTGCAATCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTTGGTGA 280
DB 317 CCTGTGGCCCTCAAGTGCAATCCCAAGAGGCCCTCCGGGGCAAGGAGGCCCTTGGTGA 376

QY 281 GAATGAGATCGGCTACTTCGCAAGATCAGCCATCCCAACATTTGGCTCTGGAGGACGT 340
DB 377 GAACGAGATCGAGTGTCTCGGTAGGATCAGTCACCCCAACATCGCTCTCGGAGGATGT 436

QY 341 CCATGAGATGCTTCTCATCTCTACTTGGCCATGAGTGGTAAACAGTGTGAACCTGTT 400
DB 437 CCACGAGAGCCCTTCCACCTTACCTGGCCATGGAACCTGTGACGGGTGGCGAGCTGT 496

QY 401 TGACCGCATCATGAGCGGGGCTCTTACACAGAAAGACGCCAGCCACCTTTGAGGGCA 460
DB 497 TGACCGCATCATGAGCGGGGCTCTTACACAGAAAGGATGCCAGCCATCTGTGGGTCA 556

QY 461 GGTCCTTGGGCTGTCTCTACCTTCATAGCTGGGCATCGTGCAACCGGGACCTCAAGCC 520

Db 557 GGTCTTGGGCGCTCTCTCTACTCTGACAGCCTGGGATCGTGACCGGACCTCAAGCC 616
QY 521 TGAACACCTCTCTATGCAACACCTTTTGGAGACTCCAAGATCATGCTCTCTGACTTTGG 580
Db 617 CGAAGACCTCTCTGATGATGCCACGCTTTGAGGACTCGAAGATCATGCTCTCTGACTTTGG 676
QY 581 CTGTCTCAAAATACAGCTGGGCAACATGCTAGGCACAGCCTGTGGGACCCCGAGATATGT 640
Db 677 ACTCTCCAAATCCAGGCTGGGAACATGCTAGGCACCGCTGTGGGACCCCTGGATATGT 736
QY 641 GGCCCCAGAGCTCTCTGAGCAGAAACCTTACGGGAAGCCGTAGATGTGTGGGCCCTTGGG 700
Db 737 GGCCCCAGAGCTCTCTGAGCAGAAACCTTACGGGAAGCCGTAGATGTGTGGGCCCTTGGG 796
QY 701 TGTCTATCTCTACATCTCTGTGTGGGTACCCCTCTTCTATGATGAGAGCGATCTGA 760
Db 797 CGTCATCTCTCTACATCTCTGTGTGGGTACCCCTCTTCTAGACGAGAGCGACCTGA 856
QY 761 ACTCTTACGCCAGATTTCTGAGGCCAGCTATGATGTTGACTCCCTTTTGGGATGACAT 820
Db 857 GCTCTTTACGCCAGATCTTCTGAGGCCAGCTATGATGTTGACTNCTCTTTCTGGGATGACAT 916
QY 821 CTCAGAAATCAGCCAAAGACTTTCATTCGCCACCTTCTGGAACGTGATCCCCAGAAAGAGTT 880
Db 917 CTCAGAAATCAGCCAAAGACTTTCATTCGCCACCTTCTGGAACGTGATCCCCAGAAAGAGTT 976
QY 881 CACCTCCAGCAGGCCCTCAGCATCTTTGGATCTCTGCGGATGTCAGCTTTGATAGGGA 940
Db 977 CACCTGCCAAAGCCCTTGGGACCTTTGGATCTTTTGGGACACACAGGCTTTGGCAGGGA 1036
QY 941 CATCTCTGGGTTCTCTCAGTCAGCAGATCCAGAAATTTTCCAGGACCCCACTGGAAGCG 1000
Db 1037 CATCTCTAGGTTTGTCTCAGTCAGCAGATCCGAAAGACTTTTGTGGACACACTGGAAGCG 1096
QY 1001 TGCATTTCATGCCACATCATTTCTCTACGTTCATCTCCGTAAGCTGGGACAAAGCCCAAGGG 1060
Db 1097 AGCTTTCATGCCACCTTGTCTCTGCGCACATCCGGAAGCTGGGCGAGATCCAGAGGG 1156
QY 1061 TGAGGAGGCTCCAGGAGGTATGACCCCTCATAGCCACCCAGGCTTGGGATAGCCA 1120
Db 1157 CGAGGGGGCTCTGAGCAGGGCATGGCCGNCACAGCCACTNAGGCCCTTGTGTGGCCA 1216
QY 1121 GTCCCCCAAGTGTGAAACACGAGTAGATCCAGGAGGAGCCAGTGGATGACTCTCCGG 1180
Db 1217 GCCCCCAAGTGTGATGTCGCCAGGNAGATGCC----GAGGCCAAGTGGANTGANCCCCAG 1272
QY 1181 TTTTCTTTTC 1190
Db 1273 ATTTCITTC 1282

RESULT 6
ADL06429
ID ADL06429 standard; cDNA; 1282 BP.
XX
AC ADL06429;
XX
DT 20-MAY-2004 (first entry)
XX
XX Human tumour-associated antigenic target (TAT) cDNA sequence #9.
XX
XX Human; tumour-associated antigenic target; TAT; cell death; tumour;
XX cancer; cytostatic; gene; ss.
XX
XX Homo sapiens.
XX
XX W02004016225-A2.
XX
XX 26-FEB-2004.
XX
XX 19-AUG-2003; 2003WO-US025892.
XX
```

PR 19-AUG-2002; 2002US-0404809P.  
PR 21-AUG-2002; 2002US-0405645P.  
PR 23-SEP-2002; 2002US-0413192P.  
PR 15-OCT-2002; 2002US-0419008P.  
PR 15-NOV-2002; 2002US-0426847P.  
PR 02-JUN-2003; 2003US-0484959P.  
XX (GETH ) GENENTECH INC.  
XX Desauvage FJ, Frantz G, Hillan KJ, Polakis P, Polson A, Smith V;  
PI Spencer SD, Wu TD, Zhang Z;  
XX WPI; 2004-257144/24.  
DR P-PSDB; ADL06509.  
XX  
XX New antibody that binds to a tumor-associated antigenic target (TAT)  
PT polypeptide, useful for preparing a composition for diagnosing or  
PT treating cancer.  
XX  
XX Claim 1; SEQ ID NO 9; 319pp; English.  
XX  
XX The present invention relates to the isolation of human tumour-associated  
CC antigenic target (TAT) polynucleotide and polypeptide sequences. Also  
CC disclosed is an antibody that binds to a TAT polypeptide. The antibody is  
CC a monoclonal antibody, an antibody fragment, a chimeric antibody or a  
CC humanised antibody. It is conjugated to a growth inhibitory agent. It is  
CC produced in bacteria or in CHO cells and induces death of a cell to which  
CC it binds. The antibody is useful for preparing a composition for  
CC diagnosing or treating tumours and cancer. The present sequence  
CC represents a human TAT cDNA sequence of the invention.  
XX  
SQ Sequence 1282 BP; 275 A; 370 C; 383 G; 245 T; 0 U; 9 Other;  
  
Query Match 54.3%; Score 844.4; DB 12; Length 1282;  
Best Local Similarity 86.2%; Pred. No. 2.8e-212;  
Matches 940; Conservative 1; Mismatches 145; Indels 4; Gaps 1;  
  
QY 101 AGACATGCTGCTCAAGAAACACAGCGAGGACATCAGCAGTGTCTATGAGATCCGGGA 160  
DB |||||  
DB 197 AAACATGCTGCTGAAGAAACACAGCGAGGACATCAGCAGCGTCTACGAGATCCGGA 256  
  
QY 161 GAAGCTGGCTCGGGTGGCTTCTCTGAGGTGATGCTGGGCCAGGAAAGGGCTCTGTCTCA 220  
DB |||||  
DB 257 GAGCTCGGCTCGGGTGGCTTCTCCGAGGTGGTCTGGCCCCAGGAGCGGGCTCCGCACA 316  
  
QY 221 TCTGTGGCCCTCAAGTGCATTCCCAAGAACACTTCGGGGCAAGGAGGCCCTGGTGA 280  
DB |||||  
DB 317 CCTGTGGCCCTCAAGTGCATTCCCAAGAACAGGCCCTCCGGGGCAAGGAGGCCCTGGTGA 376  
  
QY 281 GAATGAGATCGCGTACTTCGCAGAAATCCAGCATCCCAACATTTGTGGCTCTGGAGGACGT 340  
DB |||||  
DB 377 GAACGAGATCGCAGTGTCTCGTAGGATCAGTCAACCCCAACATCTCGCTCTGGAGGATGT 436  
  
QY 341 CCATGAGAGTCTTCTCATCTCTATTCTGGCCATCGAGCTGGTAAACAGTGGTGAACGTGT 400  
DB |||||  
DB 437 CCACGAGAGCCCTTCCCAACCTTCACTACCTGGCCATGGAACCTGGTGACGGGTGGCGAGCTGT 496  
  
QY 401 TGACCGCATCATGAGCGGGGCTCTACACAGAGAGGACCGCCAGCCACTTGTAGGGCA 460  
DB |||||  
DB 497 TGACCGCATCATGAGCGGGGCTCTACACAGAGAGGATGCCAGCCATCTTGTGGGTCA 556  
  
QY 461 GGTCTTGGCGCTGTCTCTACCTTCTATAGCTGGGATCTGTGACCGGGACCTCAAGCC 520  
DB |||||  
DB 557 GGTCTTGGCGCTGTCTCTACCTTCTATAGCTGGGATCTGTGACCGGGACCTCAAGCC 616  
  
QY 521 TGAACACCTCTCTATGCCACACCTTTTGGAGACTCCAAGATCATGTCTCTGACTTTGG 580  
DB |||||  
DB 617 CGAAACCTCTGTATGCCAGCCCTTTGAGGACTCGAAGATCATGTCTCTGACTTTGG 676  
  
QY 581 CCTGTCCAAATACAGAGTGGCAATGCTAGGACAGCCCTGTGGGACCCAGGATATGT 640  
DB |||||  
DB 677 ACTCTCAAAATACAGGCTGGGAACATGCTAGGACACCGCCTGTGGGACCCCTGGATATGT 736

QY 641 GGCCCCAGAGCTCCTGAGCAGAGAAACCTACGGGAAGCCGTAGATGTGTGGGCCCTGGG 700  
DB |||||  
DB 737 GGCCCCAGAGCTCCTTGGAGCAGAAACCTACGGGAAGCCGTAGATGTGTGGGCCCTGGG 796  
  
QY 701 TGTCACTCTCTACATCCTGCTGTGTGGTACCCCTCTCTATGATGAGAGCGATCTGA 760  
DB |||||  
DB 797 CGTCATCTCTACATCCTGCTGTGTGGTACCCCTCTCTACGAGAGCGACCTTGA 856  
  
QY 761 ACTCTTCAGCCAGATTCTGAGGGCCAGCTATGAGTTTGAAGTCTCCCTCTTGGGATGACAT 820  
DB |||||  
DB 857 GCTCTTCAGCCAGATCTGAGGGCCAGCTATGAGTTTGAAGTCTCTTCTGGGATGACAT 916  
  
QY 821 CTCAGAAATCAGCCAAAGACTTTCATTCGCCACCTTCTTGGAAAGCTGATCCCCAAGAGAGTT 880  
DB |||||  
DB 917 CTCAGAAATCAGCCAAAGACTTTCATTCGCCACCTTCTTGGAAAGCTTTCAGAAAGAGTT 976  
  
QY 881 CACTGCGCAGCAGCCCTCAGAGATCTTGGATCTCTGGGATCTCTGGGATCAGCCCTTCGATAGGGA 940  
DB |||||  
DB 977 CACCTGCCAAAGCCCTTGGGGACCTTGGATCTTGGGACACAGGCTTTGGCAGGGA 1036  
  
QY 941 CATCTCTGGTCTCTGCTAGTGAGCAGATCCAGAAAGATTTTGGCAGGACCCCACTGGAAGCG 1000  
DB |||||  
DB 1037 CATCTTAGGTTTGTCTAGTGAGCAGATCCGGAAGAACTTTGCTTGGACACTGGAAGCG 1096  
  
QY 1001 TGCAATCAATGCCACATCATCTTCTACATCCGTAAGCTGGGACAAAGCCCGAGAGG 1060  
DB |||||  
DB 1097 AGCCTTCAATGCCACCTTGTCTCGCCACATCCGGAAGCTGGGGCAGATCCCGAGAGG 1156  
  
QY 1061 TGAGGAGGCTCCAGGCGATGATGACCCGTATAGCCACCCAGGCTTGGGACTAGCCA 1120  
DB |||||  
DB 1157 CGAGGGGGCTCTGAGCAGGGCATTGGCCGNCACAGCCACTNAGGCTTGTGTGGCCA 1216  
  
QY 1121 GTCCCCCAAGTGGTGAAGAACAGGTAGATCCAGGAAGCCAAAGTGGACTGACTCCCGG 1180  
DB |||||  
DB 1217 GCCCCCCAAGTGGTGTGATGATCCAGGAGATGCC----GAGGCCAAGTGGANTGANCCTCAG 1272  
  
QY 1181 TTTTCTTTC 1190  
DB |||||  
DB 1273 ATTTCCTTC 1282  
  
RESULT 7  
ADM72654  
ID ADM72654 standard; cDNA; 1282 BP.  
XX  
AC ADM72654;  
XX  
XX 17-JUN-2004 (first entry)  
XX  
DE Human TASK120 polypeptide encoding cDNA (clone DNA151475).  
XX  
XX TASK; tumour-associated kinase; cytostatic; tumour;  
XX cell proliferative disorder; cancer; transgenic;  
XX chromosome identification; tissue typing; human; TASK120; gene; ss.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FT CDS 201..1232  
FT /\*tag= a  
FT /product= "TASK120"  
FT /transl\_except= (pos:1182..1184, aa: Xaa)  
FT /transl\_except= (pos:897..899, aa: Xaa)  
FT /transl\_except= (pos:1197..1199, aa: Xaa)  
FT /note= "Xaa = unknown"  
XX  
XX WO2004024063-A2.  
XX  
XX 25-MAR-2004.  
XX  
XX 05-SEP-2003; 2003WO-US027886.  
XX  
XX 11-SEP-2002; 2002US-0410166P.  
PR

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XX (GETH ) GENENTECH INC.
PA
XX
XX
XX PI Davis DP, Desauvage FJ, Wood WI, Zhang Z;
XX DR WPI; 2004-282984/26.
XX DR P-PSDB; ADM72655.
XX
XX New tumor-associated kinase nucleic acids and polypeptides, useful as
PT hybridization probes for isolating full length TASK DNA, for generating
PT transgenic animals, in chromosome identification, or for tissue typing.
XX
XX Claim 1; Fig 5; 140pp; English.
XX
CC The invention relates to tumour-associated kinase (TASK) polypeptides
CC (II) and encoding polynucleotides. An antibody, oligopeptide (siRNA) or
CC organic molecule that binds to (II) is useful for treating a mammal
CC having a tumour comprising cells expressing (II). Antagonists of TASK are
CC useful for treating or preventing a cell proliferative disorder (e.g.
CC cancer) associated with increased expression or activity of (II). The
CC TASK polynucleotides and polypeptides may be used as hybridization probes
CC for isolating full length TASK DNA, for generating transgenic animals, in
CC chromosome identification, or for tissue typing. The present sequence
CC represents a cDNA encoding a human TASK120 polypeptide.
XX
SQ Sequence 1282 BP; 275 A; 370 C; 383 G; 245 T; 0 U; 9 Other;
Query Match 54.3%; Score 844.4; DB 12; Length 1282;
Best Local Similarity 86.2%; Pred. No. 2.8e-212;
Matches 940; Conservative 1; Mismatches 145; Indels 4; Gaps 1;
QY 101 AGACATGCTCTGCTCAAGAAACAGACGGAGGACATCAGCAGTGCTCTATGAGATCCGGGA 160
DB 197 AAACATGCTGCTGTAAGAAACACACGGAGGACATCAGCAGGCTCTACGAGATCCGCGA 256
QY 161 GAGCTGGGCTCGGTCCTCTCTGAGTGATGCTGGCCGACGAAAGGGCTCTGCTCA 220
DB 257 GAGGCTCGGCTCGGGTGCTCTCTCCGAGGTGGTCTGGCCGACGAGCGGGGCTCCGCACA 316
QY 221 TCTTGTGGCCCTCAAGTGCATTCCTCAAGAAAGCACTTCGGGGCAAGGAGGCCCTTGTTGA 280
DB 317 CCTGTGGCCCTCAAGTGCATTCCTCAAGAGGCCCTTCGGGGCAAGGAGGCCCTTGTTGA 376
QY 281 GAATGAGATCGGCTACTTCGAGAAATCAGCCATCCCAATATGTGTGCTCTGAGGACGT 340
DB 377 GAACGAGATCGAGTGTCTCGTAGGATCAGTCAACCAACATCTGCTCTGAGGATGT 436
QY 341 CCATGAGATCCTTCTCATCTCTACTTGGCCATGGAGCTGTTACAGGTGTGAACCTTT 400
DB 437 CCAGGAGAGCCCTTCCCACTCTACCTGGCCATGGAACTGTGACGGGTGGCGAGCTGTT 496
QY 401 TGACCCGATCATGGAGCGGGCTCTTACAGAGAAGGACGCCACCCACCTTGTAGGGCA 460
DB 497 TGACCCGATCATGGAGCGGGCTCTTACAGAGAAGGATGTCAGCCATCTGTGGGTCA 556
QY 461 GGTCTTGGGCTGTCTCTACCTTCTAGCTTTCAGCTGGGATCGTGACCGGACCTCAAGCC 520
DB 557 GGTCTTGGGCTGTCTCTACCTTCTAGCTTTCAGCTGGGATCGTGACCGGACCTCAAGCC 616
QY 521 TGAAACCTCTCTATGCCACCTTTTGGAGCTCCAGATCATGTCTCTGACTTTGG 580
DB 617 CGAAACCTCTCTATGCCAGCCCTTTGAGGATCTCGAAGATCATGTCTCTGACTTTGG 676
QY 581 CCTGTCCAAATCAAGCTGGCAATGCTAGGCACAGCCCTGTGGGACCCCGAGATATGT 640
DB 677 ACTTCCAAATCAGGCTGGGACATGCTAGGCACCCGCTGTGGGACCCCTGGATATGT 736
QY 641 GGCCCCAGAGCTCTTGAGGAGAAACCTTACGGGAAGGCCGTAGATGTGTGGGCCCTTGG 700
DB 737 GGCCCCAGAGCTCTTGAGGAGAAACCTTACGGGAAGGCCGTAGATGTGTGGGCCCTTGG 796
QY 701 TGTCACTCTCTACATCTCTGTGTGGTATGCCCTTCTATCATGAGAGCGATCTCTGA 760
DB 797 CGTCACTCTCTACATCTCTGTGTGGGTATGCCCTTCTACGACGAGAGCGACCTGA 856
QY 761 ACTTTCAGCCAGATTTCTGAGGCCAGCTATGAGTTTGTGATCTCCCTTTTGGGATGACAT 820
DB 857 GGTCTTCAGCCAGATCTCTGAGGCCAGCTATGAGTTTGTGATCTCTCTTTGGGATGACAT 916
QY 821 CTCAGAAATCAGCCAAAGACTTTCATTCGCCACCTTCTGGAACGTTGATCCCGAAGAGGTT 880
DB 917 CTCAGAAATCAGCCAAAGACTTTCATTCGCCACCTTCTGGAACGAGACCTTCAGAAAGGTT 976
QY 881 CACCTCCAGCAGCGCCCTACAGCATCTTTGGGATCTCTGGGGATGCGAGCCTTCGATAGGGA 940
DB 977 CACCTGCCAACAGGCCCTTGGGGACCTTTGGGATCTTTTGGGACACAGGCTTTGGCAGGGA 1036
QY 941 CATCTGGGTTCTGTGAGTGCAGATCCAGAAAGAAATTTTGCAGGACCCACCTGGGAAGCG 1000
DB 1037 CATCTTAGGGTTGTGAGTGCAGATCCGGAAGAACTTTTGTCTGGACACACTGGGAAGCG 1096
QY 1001 TGCATTCAATGCCACATCTTCTACGTGCACATCCGTAAAGCTGGGACAAAGCCAGAGGG 1060
DB 1097 AGCCTTCAATGCCACCTTGTCTCGGCCACATCCGGAAGCTGGGCGAGATCCAGAGGG 1156
QY 1061 TGAGGAGGCTCTCAGGCGAGTGTATGACCCGTCTATAGCCACCCAGGCTTGGGACTAGCCA 1120
DB 1157 CGAGGGGGCTCTGAGCAGGGCATGGSCGNCACAGCCACTNAGGCCCTTCGTGCTGSCCA 1216
QY 1121 GTCCCCCAAGTGGTGAAACCCAGGTAGATGCTCAAGGAAGGCCCAAGTGGACTGATCTCCCG 1180
DB 1217 GCCCCCAAGTGGTGATGCTCCAGGNAGATGCC----GAGGCCAAGTGGANTGANCCCCAG 1272
QY 1181 TTTTCTTTTC 1190
DB 1273 ATTNTCTTNC 1282
XX
RESULT 8
ADM72236
ID ADM72236 standard; cDNA; 1282 BP.
XX
XX ADM72236;
XX
XX 17-JUN-2004 (first entry)
XX
XX Human TASK120 polypeptide encoding cDNA (clone Id DNA151475).
XX
XX TASK; tumour-associated kinase; cytostatic; tumour antigen;
XX cell proliferative disorder; cancer; transgenic; human; gene; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 201..1232
XX FT /*tag= a
XX FT /product= "TASK120"
XX
XX WO2004024064-A2.
XX
XX 25-MAR-2004.
XX
XX 05-SEP-2003; 2003WO-US027894.
XX
XX 11-SEP-2002; 2002US-0410166P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Desauvage FJ, Wood WI, Zhang Z;
XX
XX WPI; 2004-282985/26.
XX DR P-PSDB; ADM72237.
XX
XX New tumor-associated kinase nucleic acids and polypeptides, useful as
PT hybridization probes for isolating full length TASK DNA, for generating
PT transgenic animals, in chromosome identification, or for tissue typing.
PT
```



XX Claim 2; SEQ ID NO 41; 163pp; English.  
 XX The invention relates to new isolated tumour-associated kinase (TASK)  
 CC nucleic acid molecules and encoded polypeptides. Cytostatic. The  
 CC antibody, oligopeptide or organic molecule that binds to the TASK  
 CC polypeptide are useful for treating a mammal having a tumour comprising  
 CC cells expressing the polypeptide. Antagonists of TASK are useful for  
 CC treating or preventing a cell proliferative disorder (e.g. cancer)  
 CC associated with increased expression or activity of TASK polypeptide. The  
 CC TASK polynucleotides and polypeptides may be used as hybridization probes  
 CC for isolating full length TASK DNA, for generating transgenic animals, in  
 CC chromosome identification, or for tissue typing. The present sequence  
 CC represents a cDNA encoding a human TASK polypeptide.  
 XX  
 SQ Sequence 1282 BP; 275 A; 370 C; 383 G; 245 T; 0 U; 9 Other;  
 Query Match 54.3%; Score 844.4; DB 12; Length 1282;  
 Best Local Similarity 86.2%; Pred. No. 2.8e-212;  
 Matches 940; Conservative 1; Mismatches 145; Indels 4; Gaps 1;  
 101 AGACATGCTGCTCAAGAAACAGAGGAGGACATCAGCAGTGTCTATGATGCCGGA 160  
 197 AAACATGCTGCTGAGAAACACAGGAGGACATCAGCAGTGTCTATGATGCCGGA 256  
 161 GAAGCTGGGCTCGGCTGCTTCTCTGAGGTGATGCTGCCCCAGGAAAGGGCTCTGCTCA 220  
 257 GAGGCTGGGCTCGGCTGCTTCTCGAGGTGGTGTGCCCCAGGAGGGGCTCCGCACA 316  
 221 TCTTGTGGCCCTCAAGTGCATCCAGAAAGACATCCGAGGAGGAGGAGGAGGAGGAGT 280  
 317 CCTCGTGGCCCTCAAGTGCATCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 376  
 281 GAATGAGATCGGCTACTTGCAGATCAGCAGTGTGAGGAGGAGGAGGAGGAGGAGGAGT 340  
 377 GAACGAGATCGAGTGTCTCGTAGATCAGTCAACCCAGGAGGAGGAGGAGGAGGAGT 436  
 341 CCATGAGAGTCTTCTCATCTCTACTTCTGAGGATGAGTGTGAGGAGGAGGAGGAGT 400  
 437 CCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 496  
 401 TGACCGGATCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 460  
 497 TGACCGGATCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 556  
 461 GGTCTTGGGCTGCTCTTACCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 520  
 557 GGTCTTGGGCTGCTCTTACCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 616  
 521 TGAAGACCTCTCTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 580  
 617 CGAAACCTCTCTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 676  
 581 CTGTCCAAATACAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 640  
 677 ACTCTCAAAATCAGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 736  
 641 GGCCCGAGGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 700  
 737 GGCCCGAGGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 796  
 701 TGTCTATCTCTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 760  
 797 CGTCTATCTCTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 856  
 761 ACTCTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 820  
 857 GCTCTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 916  
 821 CTGAGATCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 880  
 917 CTCAGATCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 976

Qy 881 CACCTGCCAGCAGGCGCTTACAGCATCTTTGGATCTCTGGGATCAGCCTTTGATAGGA 940  
 Db 977 CACCTGCCAAACAGGCGCTTGGGACCTTTGGATCTTTTGGACACAGGCTTTGGCAGGA 1036  
 Qy 941 CATCTGGGTTCTGCTAGTGAGCAGATCCAGAAATTTTCCAGGACCCACTGGAAGG 1000  
 Db 1037 CATCTTAAAGTTTGTGAGTGAGCAGATCCGGAAGAACTTTCTTGGACACACTGGAAGG 1096  
 Qy 1001 TGCAATCAATGCCACATCATTTCTTACGTTCATCCGTAAGCTGGGACAAAGCCAGAGGG 1060  
 Db 1097 AGCTTCAATGCCACCTTTCTTCCGCGCATCCGGAAGCTGGGAGAGTCCAGAGGG 1156  
 Qy 1061 TGAGGAGGCTTCCAGGAGTGTATGACCGTCTATGACCCAGGAGGAGGAGGAGGAGT 1120  
 Db 1157 CGAGGGGCGCTCTGAGCAGGCGCATGSCCGNCACAGCCACTNAGGCGCTTCTGCTGGCCA 1216  
 Qy 1121 GTCCCCCAAGTGGTGAACCCAGGTAGTCCAGGAGGAGGAGGAGGAGGAGGAGGAGT 1180  
 Db 1217 GCGCCCAAGTGGTGTATGTCGCCAGGAGATGCC---GAGGCCAAGTGAGTGANCCCCAG 1272  
 Qy 1181 TTTTCTTTTC 1190  
 Db 1273 ATTTCCTTNC 1282  
 RESULT 9  
 AAS06711  
 ID AAS06711 standard; cDNA; 1032 BP.  
 XX AAS06711;  
 AC AAS06711;  
 DT 12-SEP-2001 (first entry)  
 XX Polynucleotide sequence encoding human protein kinase #11.  
 XX Human; protein kinase; PTK; STK; cancer; cardiovascular disease;  
 KW metabolic disorder; immune related disease; neurological disorder;  
 KW neurodegenerative disorder; inflammatory disorder; infectious disease;  
 KW reproductive disorder; gene therapy; ss.  
 XX Homo sapiens.  
 OS  
 XX WO200138503-A2.  
 FN  
 XX 31-MAY-2001.  
 PD  
 XX 22-NOV-2000; 2000WO-US032085.  
 PF  
 XX 24-NOV-1999; 99US-0167482P.  
 PR  
 XX (SUGG-) SUGEN INC.  
 PA  
 XX Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez P;  
 PI Flanagan P, Clary D;  
 XX WPI; 2001-343950/36.  
 DR P-PSDB; AAU03511.  
 XX Nucleic acids encoding human kinase polypeptides, useful for preventing  
 PT diagnosing and/or treating e.g. cancer, immune, cardiovascular and  
 PT neuronal-associated diseases, and microbial infections.  
 XX  
 XX Example 1; Fig 1; 433pp; English.  
 XX AAS06701-AAS06757 encode for novel human protein kinases #1-57. The novel  
 CC protein kinases have been identified as members of the tyrosine or  
 CC serine/threonine kinase (PTK and STK) families. The polynucleotides  
 CC encoding protein kinases and the polypeptides may be used in the  
 CC prevention, diagnosis and treatment of diseases associated with  
 CC inappropriate kinase expression. For example, they may be used to treat  
 CC cancers (especially cancers of haematopoietic origin), cardiovascular  
 CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),  
 CC immune related arthritis (e.g. rheumatoid arthritis), neurological

CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g. Parkinson's disease), inflammatory disorders (e.g. asthma), infectious disease (e.g. HIV) and reproductive disorders (e.g. infertility).  
 CC Additionally, polynucleotides encoding protein kinases may be used for gene therapy and as DNA probes in diagnostic assays. The protein kinase polypeptides may be used as antigens in the production of antibodies against the protein kinases and in assays to identify modulators of protein kinase expression and activity  
 XX  
 SQ Sequence 1032 BP; 206 A; 326 C; 307 G; 193 T; 0 U; 0 Other;  
 Query Match 53.88; Score 836.8; DB 4; Length 1032;  
 Best Local Similarity 88.28; Pred. No. 2.6e-210; Indels 0; Gaps 0;  
 Matches 910; Conservative 0; Mismatches 122;  
 105 ATGCTGCTGCTCAAGAAACAGACGAGGACATCAGCAGTGTCTATGAGATCCGGGAAAG 164  
 1 ATGCTGCTGCTGAAGAAACACACGAGGACATCAGCAGCGTCTACGAGATCCGGAGAGG 60  
 165 CTGGGCTCGGGTGCTTCTCTGAGGTGATGCTGCCCCAGGAAAGGGCTCTGCTCATCTT 224  
 61 CTGGGCTCGGGTGCTTCTCTGAGGTGCTGCTGCCCCAGGAGCGGGCTCCGCACACTC 120  
 225 GTGGCCCTCAAGTCATTCCTCCAGAAAGCACTTCGGGGCAAGGAGCCCTGTGGGAAT 284  
 121 GTGGCCCTCAAGTCATTCCTCCAGAAAGCCCTTCGGGGCAAGGAGCCCTGTGGGAAT 180  
 285 GAGATCCGGTACTTCCGAGAATCAGCAGATCCCAACATTTGGTCTGAGGAGCGTCCAT 344  
 181 GAGATCCGAGTCTCCGTAGGATCAGTCAACCAACATCGTCTGAGGAGTGTCCAC 240  
 345 GAGATCTCTCTATCTACTTGGCCATGAGTGTGTATACAGTGTGTGAACCTTTTGAC 404  
 241 GAGAGCCCTTCCCACTCTACTCGCCATGGAATCTGGTGGCGGTGGCGACTTTTGAC 300  
 405 CGCATCATGAGCGGGCTCTTACACAGAGAGAGCCAGCCACTTGTAGGCGAGTC 464  
 301 CGCATCATGAGCGGGCTCTTACACAGAGAGAGTCCAGCCACTTGTGGGTTCAGGTC 360  
 465 CTGGCGCTGTCTCTTACCTTCTAGCTTGGGATCGTGACCGGGACCTCAAGCCCTGAA 524  
 361 CTGGCGCGCTCTCTTACCTTGCACAGCTTGGGATCGTGACCGGGACCTCAAGCCGAA 420  
 525 AACTCTCTATGACCAACCTTTTGGAGACTTCCAGATCATGCTCTGACTTTGGCGTG 584  
 421 AACTCTCTATGACCAACCTTTTGGAGACTTCCAGATCATGCTCTGACTTTGGACTC 480  
 585 TCCAAATACAGTGGCAGATCTAGGCACAGCTTGGGACCCAGGATATGTGGCC 644  
 481 TCCAAATACAGTGGGAGATCTAGGCACAGCTTGGGACCCCTGGGATATGTGGCC 540  
 645 CCAGAGCTCTTGGAGCAGAAACCTTACGGGAAGCCGTAGATGTGGGCGCTGGGTGTC 704  
 541 CCAGAGCTCTTGGAGCAGAAACCTTACGGGAAGCCGTAGATGTGGGCGCTGGGTGTC 600  
 705 ATCTCTCATCTCTGCTGTGGGTGACCCCTTTCTATGATGAGAGCATCTTGAATC 764  
 601 ATCTCTCATCTCTGCTGTGGGTGACCCCTTTCTACGACGAGAGCCCTTGAGTCTC 660  
 765 TTGAGCAGATCTTGGGCGCAGCTATGAGTTTGCATCCCTTTTGGGATGACATCTCA 824  
 661 TTGAGCAGATCTTGGGCGCAGCTATGAGTTTGCATCTCTTTTGGGATGACATCTCA 720  
 825 GAATCAGCAGAAAGTCTTCAATTCGGCAGCTTCTGAAAGCTGATCCCGAAGAGGTTCACC 884  
 721 GAATCAGCAGAAAGTCTTCAATTCGGCAGCTTCTGAGGAGAGCCCGAAGAGGTTCACC 780  
 885 TGCCAGCAGGCGCTTACAGCATCTTTTGGATCTCTGGGATGAGCGCTTCTGATGGGACATC 944  
 781 TGCCAGCAGGCGCTTTCGGCAGCTTTCGGGATGAGCGCTTCTGATGGGACATC 840  
 945 CTGGGTTCTGTCAGTGAGCAGATCCAGAAAGATTTTGGCAGGACCCACTGGAAGCGTGA 1004

841 TTAGGCTCTCTCAGTCAGCAGATCCGGAAGAACTTTGCTCGGACACACTGGAACGAGCC 900  
 1005 TTCAATGCCACATCATTTCTTACCTCATCTCCTGTAAGCTGGGACAAAGCCAGAGGTGAG 1064  
 901 TTCAATGCCACCTCTGTTCTTCTGCGCCACATCCGGAAGCTGGGCGAGATCCAGAGGGGAG 960  
 1065 GAGGCTCCAGGCGAGTGTATGACCCGTCATAGCCACCCAGGCTTTGGGACTTAGCCAGTCC 1124  
 961 GGGGCTCTGAGCAGGCGATGGCCCGCCACAGGCACTCAGGCTTCCGCTGGCCAGGCC 1020  
 1125 CCCAAGTGGTGA 1136  
 1021 CCCAAGTGGTGA 1032  
 RESULT 10  
 ABZ11323  
 ID ABZ11323 standard; cDNA; 1216 BP.  
 XX ABZ11323;  
 AC ABZ11323;  
 XX  
 DT 20-JAN-2003 (first entry)  
 XX Human polynucleotide SEQ ID NO 205.  
 DE  
 XX Human; genome mapping; gene therapy; food supplement; virus; fungus;  
 cell-proliferative disorder; neurodegenerative disease; bacterial;  
 Parkinson's disease; Alzheimer's disease; autoimmune disease;  
 multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;  
 arthritis; cytostatic; immunomodulator; nontropic; neuroprotective;  
 antiparkinsonian; antidiabetic; immunosuppressive; dermatological;  
 haemostatic; vulnary; fungicide; antibacterial; virucide; protozoacide;  
 antiarthritic; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200270539-A2.  
 PN  
 XX 12-SEP-2002.  
 PD  
 XX  
 XX 05-MAR-2002; 2002WO-US005095.  
 PF  
 XX  
 XX 05-MAR-2001; 2001US-00799451.  
 PR  
 XX (HYSE-) HYSEQ INC.  
 PA  
 XX  
 PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;  
 PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;  
 PI Wehrman T, Wang J, Wang D, Drmanac RT;  
 XX  
 DR WPI; 2002-759812/82.  
 DR P-PSDB; ABP69106.  
 XX  
 XX New polynucleotides comprising sequences assembled from expressed  
 sequence tags (ESTs), useful for treating cell-proliferative, or platelet  
 neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet  
 or coagulation disorders.  
 XX  
 PS Claim 1; SEQ ID NO 205; 1012pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated polynucleotide (I) comprising a  
 nucleotide sequence selected from any of 948 sequences (ABZ11119-  
 ABZ12066) or their mature protein coding portion, active domain coding  
 protein or complementary sequences. The polynucleotides are useful for  
 identifying expressed genes or for physical mapping of human genome. The  
 encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight  
 markers, as a food supplement, for generating antibodies, in medical  
 imaging, screening and diagnostic assays and for treating cell-  
 proliferative disorders (cancer), neurodegenerative diseases (Parkinson's  
 or Alzheimer's disease), autoimmune diseases (multiple sclerosis,  
 diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,  
 platelet or coagulation disorders, wound, burns, incision, ulcers, liver  
 or lung fibrosis, infections (bacterial, viral, fungal, parasitic),

CC arthritis, etc. Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 1216 BP; 228 A; 404 C; 352 G; 232 T; 0 U; 0 Other;

Query Match 51.7%; Score 803.6; DB 6; Length 1216;  
Best Local Similarity 87.5%; Pred. No. 1.6e-201;  
Matches 892; Conservative 0; Mismatches 124; Indels 4; Gaps 1;

|    |      |   |      |
|----|------|---|------|
| Qy | 168  | GGCTCGGGTCTCTCTGAGTGATGTCGCCAGGAAGGGCTCTGCTCATCTTGTG          | 227  |
| Db | 201  | GGCAGGGGTGCTTCTCGAGTGCTGTCGCCAGGAGCGGGCTCGCACCTCGTG           | 260  |
| Qy | 228  | GCCCTCAAGTGCAATCCCAAGAAAGCACTTCGGGGCAAGAGCGCCTGGTGGAGATGAG    | 287  |
| Db | 261  | GCCCTCAAGTGCAATCCCAAGAAAGCACTTCGGGGCAAGAGCGCCTGGTGGAGACGAG    | 320  |
| Qy | 288  | ATCGCGGTACTTCGCAAGATCAGCCATCCCAACATTTGGTCTCTGGAGGAGCTCCATGAG  | 347  |
| Db | 321  | ATCGCAGTGTCTCCGTAGGATCAGTCACCCCAACATCGTCTCTGGAGGATGTCACGAG    | 380  |
| Qy | 348  | AGTCTTCTCATCTCTACTTGGCCATGAGCTGCTACAGTGTGTGAACTGTTTGACGGC     | 407  |
| Db | 381  | AGCCTTCTCCACCTCTCTACCTGGCCATGGAATGCTGAGCGGTGGCGAGCTGTTTGACGGC | 440  |
| Qy | 408  | ATCATGAGCGGGGCTCTCTACAGAGAAGAGCGCCAGCCACTTGTAGGCGAGTCTT       | 467  |
| Db | 441  | ATCATGAGCGGGGCTCTCTACAGAGAAGAGTCCAGCCATCTGTTGGTCAAGTCTT       | 500  |
| Qy | 468  | GGGCTCTCTCTACTTCTATAGCCTGGGATCGTGCACGGGACCTCAAGCCTGAAAC       | 527  |
| Db | 501  | GGGCGCGTCTCTACTCTGCAAGCCTGGGGATCGTGCACGGGACCTCAAGCCCGAAAC     | 560  |
| Qy | 528  | CTCTCTATGCCACACTTTTGGAGCTCCAGATCATGTCTCTGACTTTGGCTTCC         | 587  |
| Db | 561  | CTCTCTATGCCACCGCCCTTGGAGACTCGAAGATCATGTCTCTGACTTTGGACTTCC     | 620  |
| Qy | 588  | AAATACAAGCTGCAACATGTAGGCACAGCCTGTGGGACCCAGGATATGTGGCCCCA      | 647  |
| Db | 621  | AAATACAAGCTGGAACATGTAGGCACCGCCTGTGGGACCCCTGATATGTGGCCCCA      | 680  |
| Qy | 648  | GAGCTCTCTGAGCAGAAACCTTACGGGAAGCCCGTAGATGTGTGGGCCCTGGGTGTCATC  | 707  |
| Db | 681  | GAGCTCTTGGAGCAGAAACCTTACGGGAAGCCCGTAGATGTGTGGGCCCTGGGGTTCATC  | 740  |
| Qy | 708  | TCCTACATCTCTGTGTGGTACCCCTTCTATGATGAGGAGCATCTGAACTCTTC         | 767  |
| Db | 741  | TCCTACATCTCTGTGTGGTACCCCTTCTACGACGAGAGCGACCTTGAGCTCTTC        | 800  |
| Qy | 768  | AGCCAGATTTCTGAGGCGCAGCTATGATTTTGACTTCCCTTTTGGGATGACATCTCAGAA  | 827  |
| Db | 801  | AGCCAGATTTCTGAGGCGCAGCTATGATTTTGACTTCTCTTCTGGGATGACATCTCAGAA  | 860  |
| Qy | 828  | TCAGCCAAAGACTTTCATTCGCCACTTCTGTGAAACGTGATCCCAAGAGAGTTTCACTGTC | 887  |
| Db | 861  | TCAGCCAAAGACTTTCATTCGCCACTTCTGTGAGCGAGACCCCAAGAGAGTTTCACTGTC  | 920  |
| Qy | 888  | CAGCAGGCCCTTACAGCATCTTTTGGATCTCTGGGAGATGAGCCTTCGATAGGACATCTTG | 947  |
| Db | 921  | CAACAGGCCCTTTCGGCACCTTTTGGATCTCTGGGAGACAGAGCTTCGACAGGACATCTTA | 980  |
| Qy | 948  | GGTCTCTGAGTACGAGATCCAGAAATTTTCCAGGACCCCTGAGGCGTGCATTC         | 1007 |
| Db | 981  | GGTCTCTGAGTACGAGATCCAGAAATTTTCTCGGACACACTTGGAGCGAGCCTTC       | 1040 |
| Qy | 1008 | AATGCCACATCTTCTTACGTTCATCCGTAAGCTGGGACAAAGCCAGAGGGTGGAG       | 1067 |
| Db | 1041 | AATGCCACCTCTTCTCTCGGCCACATCCGAGAGTGGGGAGATCCAGAGGGGAGGG       | 1100 |
| Qy | 1068 | GCCTTCAGGAGTGTATGACCCCGTATAGCCACCCAGGCTTTGGATAGCCAGTCCCCC     | 1127 |
| Db | 1101 | GCCTTCAGGAGGATGGGCGGCACAGCCACTCAGGCGCTCCGTGTGGCCAGCCCCC       | 1160 |

|    |      |  |      |
|----|------|--|------|
| Qy | 1128 | AAGTGGTGAACCAAGCAGGTAGTCCAAAGGAAGCCAAAGTGACTGACTCCCGGTTTTCT  | 1187 |
| Db | 1161 | AAGTGGTGAATGCCAGGCAGATGCC-----GAGGCCNAGTGACTGACCCCGAGATTCTCT | 1216 |

RESULT 11  
ADR39798

ID ADR39798 standard; cDNA; 1180 BP.

XX ADR39798;

DT 18-NOV-2004 (first entry)

XX Human kinase and phosphatase KPP-25 encoding cDNA SEQ ID NO:71.

human; kinase and phosphatase protein; KPP; enzyme; cytosolic;  
antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective;  
cerebroprotective; anti-HIV; antiallergic; antiinflammatory;  
thyromimetic; gene therapy; cell proliferative disorder; cancer;  
atherosclerosis; neurological disorder; epilepsy; Huntington's disease;  
stroke; immune disorder; inflammatory disorder; AIDS; allergy;  
developmental disorder; Hypothyroidism; Cushing's syndrome; infection;  
KPP-25; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 19..1137

XX /\*tag= a

/product= "kinase and phosphatase KPP-25"

XX WO2004074453-A2.

XX 02-SEP-2004.

XX 20-FEB-2004; 2004WO-US005092.

XX 20-FEB-2003; 2003US-0449059P.

XX 19-MAR-2003; 2003US-0456932P.

XX 28-MAR-2003; 2003US-0458844P.

XX 09-APR-2003; 2003US-0461678P.

XX 17-APR-2003; 2003US-0463937P.

XX (INCY-) INCYTE CORP.

XX Ramkumar J, Marquis JP, Swarnakar A, Chawla NK, Tran UK;

XX Becha SD, Lee SY, Hafalia AJA, Richardson TW, Khare R, Jiang X;

XX Jackson AA, Yang J, Gorvad AE;

XX WPI; 2004-635568/61.

XX P-PSDB; ADR39752.

XX New human kinases and phosphatases (KPP) for diagnosing, treating and  
preventing diseases or conditions associated with aberrant KPP expression  
e.g. cancer, acquired immunodeficiency syndrome, epilepsy, or infections.

XX Claim 5; SEQ ID NO 71; 299pp; English.

XX The present sequence encodes the human kinase and phosphatase protein  
(KPP), designated KPP-25. The human KPP sequences from the present  
invention have cytosolic, antiarteriosclerotic, anticonvulsant,  
nootropic, neuroprotective, cerebroprotective, anti-HIV, antiallergic,  
antiinflammatory and thymimetic activities, and can be used in gene  
therapy. The human KPP proteins and polynucleotides can be used in  
diagnosing, treating and preventing diseases or conditions associated  
with the decreased expression or overexpression of KPP, such as cell  
proliferative (e.g. cancer, atherosclerosis), neurological (e.g.  
epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS,  
allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome)  
disorders, or infections. They can also be used in assessing the effects  
of exogenous compounds on the expression of nucleic acid and amino acid  
sequences of KPP. The KPP or its fragments are useful in screening

|  |   |
|--|---|
| CC compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the target polynucleotide and compounds that specifically bind to or modulate the activity of the polypeptide. |   |
| XX   | Sequence 1180 BP; 230 A; 393 C; 336 G; 221 T; 0 U; 0 Other;             |
| Query Match 51.5%; Score 800.2; DB 13; Length 1180; Best Local Similarity 87.5%; Pred. No. 1.3e+200; Matches 888; Conservative 0; Mismatches 123; Indels 4; Gaps 1;  |   |
| Qy   | 168 GGCTCGGGTGCCTTCTCTGAGGTGATGCTGCGCCAGGAAAGGGGCTCTGCTCATCTGTG 227     |
| Db   | 169 GGCAGGGTGCCTTCTCCGAGGTGGTGTGCGCCAGGAGCGGGCTCCGCACCTCGTG 228         |
| Qy   | 228 GCCTCAAGTGCAATCCCAAGAACACTTTCGGGGCAAGGAGGCCCTGTGGAGATGAG 287        |
| Db   | 229 GCCTCAAGTGCAATCCCAAGAGGCCCTCCGGGGCAAGGAGGCCCTGTGGAGACGAG 288        |
| Qy   | 288 ATCGCGTACTTCGAGAAATCAGCCATCCCAACATTTGGCTCTGGAGGAGCTCCATGAG 347      |
| Db   | 289 ATCGCAGTGTCCGTAGGATCAGTCAACCAACATGCTGCTCTGGAGGATGTCACGAG 348        |
| Qy   | 348 AGTCCTTCTCATCTCTACTTTGGCCATGGAGCTGCTAAAGTGGTGAACCTTTGACCGC 407      |
| Db   | 349 AGCCTTCCCACTTACTTGGCCATGGAACTGGTGACGGGTGGGAGCTGTTTGACCGC 408        |
| Qy   | 408 ATCATGAGCGGGCTCCTTACACAGAGAAGAGCCAGCCACTTTGTAGGCGAGGTCCTT 467       |
| Db   | 409 ATCATGAGCGGGCTCCTTACACAGAGAAGAGTCCAGCCACTTGTGTGGTTCAGGTCCTT 468     |
| Qy   | 468 GGGCTGTCTCTACCTTCTATAGCTGGGATCGTGACCGGACCTCAAGCCCTGAAAC 527         |
| Db   | 469 GGGCGCGTCTCTACCTTCTGACAGCTGGGGATCGTGACCGGGACCTCAAGCCCGAAAC 528      |
| Qy   | 528 CTCTCTATGCCACACCTTTTGGAGCTTCAAGATCATGTCTCTGACTTTGGCTCTGCC 587       |
| Db   | 529 CTCTGTATGCCAGCCCTTTGAGACTTCGAGATCATGTCTCTGACTTTGGACTCTCC 588        |
| Qy   | 588 AAATACAAGCTGGCAACATGCTAGGCACACCTGTGGGACCCAGGATATGTGGCCCCA 647       |
| Db   | 589 AAATCCAGGCTGGGAACATGTAGGCACACCGCTGTGGGACCCCTGGATATGTGGCCCCA 648     |
| Qy   | 648 GAGCTCTGGAGCAGAACCTTACGGAGCGCTAGATGTGTGGGCGCTGGGTGTATC 707          |
| Db   | 649 GAGCTCTGGAGCAGAACCTTACGGAGCGCTAGATGTGTGGGCGCTGGGGGTATC 708          |
| Qy   | 708 TCCTACATCTCTGTGTGGGTACCCCTTCTATGATGAGAGCGATCTCTGAACTCTTC 767        |
| Db   | 709 TCCTACATCTCTGTGTGGGTACCCCTTCTACGACGAGCGACCTTGACTCTTC 768            |
| Qy   | 768 AGCCAGATCTGAGGGCCAGCTATGAGTTGACTCCCTTTTGGGATGACATCTCAGAA 827        |
| Db   | 769 AGCCAGATCTGAGGGCCAGCTATGAGTTGACTCTCTTCTGGGATGACATCTCAGAA 828        |
| Qy   | 828 TCAGCCAAAGACTTTCATCGCCACTTCTGGAAGTATCCCAAGAGAGTTTCACTGTC 887        |
| Db   | 829 TCAGCCAAAGACTTTCATCGCGACCTTCTGAGCGAGACCCCAAGAGAGTTTCACTGTC 888      |
| Qy   | 888 CAGCAGCCCTTACAGCATCTTTGGATCTCTGGGATGCGAGCTTTCGATAGGACATCTG 947      |
| Db   | 889 CAACAGGCTTTCGGGCACTTTTGGATCTCTGGGAGACAGGCTTTCGACAGGACATCTTA 948     |
| Qy   | 948 GGTTCGTGAGTGAGCAGATCCAGAAGAAATTTTCCAGGAGCCCACTGGAAGCGTGCAATC 1007   |
| Db   | 949 GGCTCTGTGAGTGAGCAGATCCGGAAGAACTTTTCTCGGACACACTGGAAGCGAGCTTC 1008    |
| Qy   | 1008 AATGCCATCATCTTCTACGTCACTCGTAACTGGGACAAAGCCAGAGGGGTGAGAG 1067       |
| Db   | 1009 AATGCCACCTCTGTTCCTGCGCCACATCCGGAAGCTGGGGCAGATCCCAAGAGGGCGAGG 1068  |
| Qy   | 1068 GCCTCCAGGAGTGTATGACCCGTTCATAGCCACCCAGGCGCTTGGGACTAGGCACTGCCCC 1127 |
| Db   | 1069 GCCTCTGAGCAGGCGCATGGCCCGCACAGCCACTCAGGCGCTCCGTGTGGCCAGCCCCC 1128   |

|    |  |
|----|--|
| Qy | 1128 AAGTGTGAAACACAGGTAGATCCCAAGGAGGCCAAGTGGACTGACTCCGGTT 1182   |
| Db | 1129 AAGTGTGTATGCCAGGCAGATGCC----GAGGCCAAGTGGACTGACCCCGAGAT 1179 |

RESULT 12

ACC46211 standard; cDNA; 1656 BP.

AC ACC46211;

DT 02-JUN-2003 (first entry)

XX Human dithp intracellular signalling protein-encoding cDNA.

Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis; cancer; cell proliferative disorder; autoimmune disorder; inflammatory disorder; infection; hormonal disorder; metabolic disorder; neurological disorder; gastrointestinal disorder; transport disorder; connective tissue disorder; drug screening; proteome analysis; gene therapy; antisense therapy; genotyping; transgenic animal; knock in; disease model; toxicological testing; transcript imaging; intracellular signalling; gene; ss.

XX Homo sapiens.

XX WO200297031-A2.

XX 05-DEC-2002.

XX 27-MAR-2002; 2002WO-US010056.

XX 28-MAR-2001; 2001US-0279619P.

XX 29-MAR-2001; 2001US-0280067P.

XX 16-MAY-2001; 2001US-0291280P.

XX 17-MAY-2001; 2001US-0291829P.

XX 19-MAY-2001; 2001US-0291849P.

XX 20-JUN-2001; 2001US-0299776P.

XX 20-JUN-2001; 2001US-0300001P.

XX (INCY-) INCYTE GENOMICS INC.

XX Daifo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;

XX Dufour GH, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;

XX Doughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;

XX Paralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;

XX Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;

XX WPI; 2003-129518/12.

XX P-PSDB; ABR41269.

XX Novel human diagnostic and therapeutic polypeptide useful for identifying test compound which specifically binds to a polypeptide encoded by human diagnostic and therapeutic polynucleotide, and to induce antibodies.

XX Claim 2; SEQ ID NO 132; 591pp; English.

XX The invention relates to novel human diagnostic and therapeutic polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded proteins (DITHP; ABR41136-ABR41812). The invention also relates to polynucleotide sequences at least 90% identical to the dithp cDNA sequences of the invention; recombinant vectors, host cells and transgenic organisms comprising a dithp nucleic acid sequence; the recombinant production of DITHP proteins; antibodies specific for DITHP proteins; microarrays comprising dithp nucleic acid sequences; methods of detecting dithp nucleotide and protein sequences; methods of screening for compounds which specifically bind a DITHP protein; and methods of assessing the toxicity of test compounds using a dithp hybridisation probe. Dithp nucleic acid sequences and DITHP proteins may be used in the diagnosis of a wide variety of conditions including cancer and other cell

CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,  
 CC viral, fungal or parasitic infections; hormonal disorders; metabolic  
 CC disorders; neurological disorders; gastrointestinal disorders; transport  
 CC disorders; and connective tissue disorders. They may also be used to  
 CC screen for modulators of protein activity or gene expression. DITHP  
 CC proteins can additionally be used in analysis of the proteome of a tissue  
 CC or cell type and to induce antibodies. The dithp nucleic acids are  
 CC additionally useful in somatic or germline gene therapy of the disorders  
 CC mentioned above, as a source of antisense sequences, as a source of  
 CC probes and primers, in genotyping and identification of individuals, in  
 CC the generation of transgenic animal models of human disease or knock in  
 CC humanised animals, in toxicological testing, and in transcript imaging.  
 CC The present sequence represents a dithp cDNA encoding a DITHP protein  
 CC which has intracellular signalling activity. Note: The sequence data for  
 CC this patent did not form part of the printed specification, but was  
 CC obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX

SQ Sequence 1656 BP; 301 A; 515 C; 502 G; 338 T; 0 U; 0 Other;

Query Match 45.0%; Score 699; DB 8; Length 1656;  
 Best Local Similarity 77.5%; Pred. No. 7.7e-174;  
 Matches 920; Conservative 0; Mismatches 240; Indels 27; Gaps 5;

Qy 380 GGTAAAGAGGTGGTGAACCTTTTGACCGCATCATGGAGCGGGCTCTACACAGAGAAGGA 439  
 Db 462 GGTGACGGGTGGCGAGCTGTTTGACCGCATCATGGAGCGGGCTCTACACAGAGAAGGA 521  
 Qy 440 CGCCAGGACCTTGTAGGCGAGTCTTGGCGGTCTCTACCTTATGACCTTGGGAT 499  
 Db 522 TGCCAGGACCTTGTGGGTGAGGTCTTGGCGGTCTCTACCTTATGACCTTGGGAT 581  
 Qy 500 CGTGACCGGACCTCAAGCCTGAAACCTCTCTATGCCACACCTTTTGGAGGACTCCAA 559  
 Db 582 CGTGACCGGACCTCAAGCCTGAAACCTCTCTATGCCACACCTTTTGGAGGACTCGAA 641  
 Qy 560 GATCATGGTCTCTGACCTTTGGGCTGTGCAAAATCAAGCTGGCAACATGCTAGGACAGC 619  
 Db 642 GATCATGGTCTCTGACCTTTGGGCTGTGCAAAATCAAGCTGGCAACATGCTAGGACAGC 701  
 Qy 620 CTGTGGGACCCAGGATATGTGGCCCGCCAGACTCTGTGGAGCAGAAACCTTACGGGAAGGC 679  
 Db 702 CTGTGGGACCCCGATATGTGGCCCGCCAGACTCTGTGGAGCAGAAACCTTACGGGAAGGC 761  
 Qy 680 CGTAGATGTGTGGGCTGTGCTCTACATCTCTGCTGTGTGGTACCCCTT 739  
 Db 762 CGTAGATGTGTGGGCTGTGCTCTACATCTCTGCTGTGTGGTACCCCTT 821  
 Qy 740 CTATGATGAGAGCGATCTGAACTCTTTCAGCCAGATCTGAGGCGCAGCTATGAGTTGA 799  
 Db 822 CTACGACGAGAGCGACCTGAGCTCTTTCAGCCAGATCTTGTGGGCGCAGCTATGAGTTGA 881  
 Qy 800 CTCCCTCTTTTGGATGACATCTCAGATCAGCCAAAGACTTTCATTCGCCACCTTCTGGA 859  
 Db 882 CTCTCTCTTTTGGATGACATCTCAGATCAGCCAAAGACTTTCATTCGCCACCTTCTGGA 941  
 Qy 860 ACGTGATCTCCAGAGAGGTTTCACTGCGCAGCGCCCTACGACATCTTTGGATCTCTGG 919  
 Db 942 GCGAGACCCCGAAGAGGTTTCACTGCGCAGCGCCCTTTCGCCACCTTTCGATCTCTGG 1001  
 Qy 920 GGATGACGCTTTCGATAGGAGCATCTTGGGTTCTGTGAGTGAGCAGATCCAGAGAATTT 979  
 Db 1002 GGACACAGCTTTCGACAGGAGCATCTTAGGCTCTGTGAGTGAGCAGATCCGGAAGACTT 1061  
 Qy 980 TGCAGAGACCTTGGAGCGGTGATTAATGCGACATCATCTTCTAGTCACATCCGTAA 1039  
 Db 1062 TGCTCGGACACATCTGGAAGCGAGCTTCAATGCGACCTCTGTTCTTGGCGCCACATCCGGA 1121  
 Qy 1040 GCTGGGACAAAGCCGAGGAGGAGGCTTCCAGCGCATGTATGACCGTCATAGCCA 1099  
 Db 1122 GCTGGGAGATCCAGAGGCGGAGGGGCTCTTGAGCAGGCGCATGCGCCGACAGCCA 1181  
 Qy 1100 CCCAGGCTTTGGGACTAGCCAGTCCCCCAAGTGGTGAACACAGGTAGATGCCAAGGAAG 1159

Db 1182 CTACAGGCTCTCGTCTGGCCAGCCGCCCAAGTGTGTATGCCAGCAGATGCC-----GAG 1237  
 Qy 1160 GCCAAGTGGATGACTCCCGTCTTTTCTTCTCCAGCCCTTTTGGTCTCTTTCTGTGAT 1219  
 Db 1238 GCCAAGTGGATGACTGACCCCGCCAGATTTCTTCTTGGATGCTTTCGGTCCCTCCCAAC 1297  
 Qy 1220 CTTTGTCTCTCAGACTGGCCTCTGCTGGAAGTCTGA-GACTGGGTGTGATGATGGCAC 1278  
 Db 1298 CCCTCCCTGGGCTGGCCTCTGCTGGAATTTGAGATTTGAGGGTGTGGCGCATGGCGC 1357  
 Qy 1279 TAGGGT-----ACGGGGCTTCCCAAGTATGTCCCGCAGCCTCTATTCTTACCTATGGTGA 1334  
 Db 1358 TGGGGTTGGAATGGGGCACCCCAAGTGTGTCCCGCAGGCTCTGCCCTCGCTGGGGCAGT 1417  
 Qy 1335 GGCTCCCTTTCCCATGTGCGTCCGACCATCTCTATGGAACATGAGGAGGTGTTCAAAAGTGG 1394  
 Db 1418 GGCTCCCTCTCCCTGTGGCTCTCCCGCCCTGCGCCCGCCCGCCCAAAAGCCGAGG 1477  
 Qy 1395 ACTTGGGAGCCATCTTCTCTGACCTTGTGCAACACATGATGCTTGTGGCTGTCTGTG 1454  
 Db 1478 GGGTGTCTGGCAGCGGGCC-----TCAGGGGCTGTCTTCTGCGCGCTGTGTGTG 1530  
 Qy 1455 CTTTGTGCTGCTGGGTGGTCTGCTGCTGTGTGTGGCCCTTTTAGTCTCTCC----- 1505  
 Db 1531 CTTGCTGAGTGTGGGTGGTCTGCTGCTGTGTGTGTCATGTGTCATGGCTTCCAGCCCTCCAG 1590  
 Qy 1506 --TTTTCTTAACCAATAAAGCAACCAAGCAACCAAAACCAAAACCAAA 1550  
 Db 1591 TTTTCCCAACCAATAAAGCAACCAAGCAACCAAAACCAAAACCAAA 1637

RESULT 13  
 ACC46241  
 ID ACC46241 standard; cDNA; 1371 BP.  
 XX AC ACC46241;  
 XX DT 02-JUN-2003 (first entry)  
 XX DE Human dithp intracellular signalling protein-encoding cDNA.  
 XX KW Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;  
 KW cancer; cell proliferative disorder; autoimmune disorder;  
 KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;  
 KW neurological disorder; gastrointestinal disorder; transport disorder;  
 KW connective tissue disorder; drug screening; proteome analysis;  
 KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;  
 KW disease model; toxicological testing; transcript imaging;  
 KW intracellular signalling; gene; ss.  
 XX OS Homo sapiens.  
 XX FN WO200297031-A2.  
 XX PD 05-DEC-2002.  
 XX PF 27-MAR-2002; 2002WO-US010056.  
 XX PR 28-MAR-2001; 2001US-0279619P.  
 XX PR 29-MAR-2001; 2001US-0280067P.  
 XX PR 29-MAR-2001; 2001US-0280068P.  
 XX PR 16-MAY-2001; 2001US-0291280P.  
 XX PR 17-MAY-2001; 2001US-0291829P.  
 XX PR 17-MAY-2001; 2001US-0291849P.  
 XX PR 19-JUN-2001; 2001US-0299428P.  
 XX PR 20-JUN-2001; 2001US-0299776P.  
 XX PR 20-JUN-2001; 2001US-0300001P.  
 XX (INCY-) INCYTE GENOMICS INC.  
 XX PA Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;  
 XX PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshay SR;

PI Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;  
PI Paralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;  
PI Flores V, Marwaha R, Lo A, Lan RV, Urashka M;  
XX WPI; 2003-129518/12.  
DR P-PSDB; ABR41299.  
XX  
XX Novel human diagnostic and therapeutic polypeptide useful for identifying  
PT test compound which specifically binds to a polypeptide encoded by human  
PT diagnostic and therapeutic polynucleotide, and to induce antibodies.  
XX  
XX Claim 2; SEQ ID NO 162; 591pp; English.  
XX  
XX The invention relates to novel human diagnostic and therapeutic  
CC polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded  
CC proteins (DITHP; ABR41136-ABR41812). The invention also relates to  
CC polynucleotide sequences at least 90% identical to the dithp cDNA  
CC sequences of the invention; recombinant vectors, host cells and  
CC transgenic organisms comprising a dithp nucleic acid sequence; the  
CC recombinant production of DITHP proteins; antibodies specific for DITHP  
CC proteins; microarrays comprising dithp nucleic acid sequences; methods of  
CC detecting dithp nucleotide and protein sequences; methods of screening  
CC for compounds which specifically bind a DITHP protein; and methods of  
CC assessing the toxicity of test compounds using a dithp hybridisation  
CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the  
CC diagnosis of a wide variety of conditions including cancer and other cell  
CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,  
CC viral, fungal or parasitic infections; hormonal disorders; metabolic  
CC disorders; neurological disorders; gastrointestinal disorders; transport  
CC disorders; and connective tissue disorders. They may also be used to  
CC screen for modulators of protein activity or gene expression. DITHP  
CC proteins can additionally be used in analysis of the proteome of a tissue  
CC or cell type and to induce antibodies. The dithp nucleic acids are  
CC additionally useful in somatic or germline gene therapy of the disorders  
CC mentioned above, as a source of antisense sequences, as a source of  
CC probes and primers, in genotyping and identification of individuals, in  
CC the generation of transgenic animal models of human disease or knock in  
CC humanised animals, in toxicological testing, and in transcript imaging.  
CC The present sequence represents a dithp cDNA encoding a DITHP protein  
CC which has intracellular signalling activity. Note: The sequence data for  
CC this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 1371 BP; 246 A; 441 C; 412 G; 272 T; 0 U; 0 Other;

Query Match 43.9%; Score 681.8; DB 8; Length 1371;  
Best Local Similarity 78.4%; Pred. No. 2.5e-169;  
Matches 885; Conservative 0; Mismatches 227; Indels 17; Gaps 5;

Qy 380 GGTAAACAGGTGGTGAACCTTTTGGACCGCATCATGAGCGGGGCTCTTACACAGAGAAGGA 439  
Db 211 GGTACGGGTGGCGAGCTGTTTGAACCGCATCATGAGCGGGGCTCTTACACAGAGAAGGA 270

Qy 440 CGCCAGACA-CTTTGTAGGAGGAGCTCTTGGCGCTGCTCTTACATGAGCTGGCA 498  
Db 271 TGCCAGGCATCTCTGGTGGGTGAGGTCTTGGCGCGCTCTTCTTACCTGACAGCTGGGA 330

Qy 499 TCGTGCCCGGGAGCTCAAGCTGTAAGAACCTCTCTATGCCACACCTTTTGGAGACTCCA 558  
Db 331 TCGTGCCCGGGAGCTCAAGCCCGGAAACCTCTCTATGCCACACCTTTTGGAGACTCGA 390

Qy 559 AGATCATGGTCTCTGACTTTGGCTGTGTCACAAATACAAAGCTGGCAACATGTAGGCAAG 618  
Db 391 AGATCATGGTCTCTGACTTTGGCTGTGTCACAAATACAAAGCTGGCAACATGTAGGCAAG 450

Qy 619 CCTGTGGAGCCCAAGGATATGTCGCCCGCAGAGCTCTTGGAGCAGAAACCTTACGGGAGG 678  
Db 451 CCTGTGGAGCCCAAGGATATGTCGCCCGCAGAGCTCTTGGAGCAGAAACCTTACGGGAGG 510

Qy 679 CCGTAGATGTGTGGGCGCTGGGTGTCTCTTACATCTCTCTTACATCTCTGTGTGGGTACCCCGCT 738  
Db 511 CCGTAGATGTGTGGGCGCTGGGTGTCTCTTACATCTCTCTTACATCTCTGTGTGGGTACCCCGCT 570

Qy 739 TCTATCATGAGAGCGATCCTGAACCTCTTACAGCCAGATTCTTGAGGGCCAGCTATGAGTTTG 798  
Db 571 TCTACGACGAGAGCGAGCCCTTGAGCTCTTTCAGCCAGATCTCTTGAGGGCCAGCTATGAGTTTG 630

Qy 799 ACTTCCCCCTTTTGGGATGACATCTCAGAACTCAGCAAGAACTTCATTCGCGCACCTTCTGG 858  
Db 631 ACTTCTCTTCTGGGATGACATCTCAGAACTCAGCAAGAACTTCATTCGCGCACCTTCTGG 690

Qy 859 AACGTGATCCCAAGAGAGGTTTCACTTGCAGAGGCGCTTACAGCATCTTTTGGATCTCTG 918  
Db 691 AGCGAGACCCCAAGAGAGGTTTCACTTGCAGAGGCGCTTTCGCGCACCTTGGATCTCTG 750

Qy 919 GGGATGAGCGCTTCGATAGGAGCATCTTGGGTTCTGCTAGTGAGCAGATCCAGAGAAATT 978  
Db 751 GGGACACAGCGCTTCGACAGGAGCATCTTAGGCTCTGTCAGTGAGCAGATCCGGAAGAACT 810

Qy 979 TTGCCAGGACCCACTGGAAGCGTGCTTCAATGCCACATCATTTCTTACGTACACATCCGTA 1038  
Db 811 TTGCTGGACACACTGGAAGCGAGCTTCAATGCCACCTGTTCTTCTGGCCACATCCGGA 870

Qy 1039 AGTGGGACAAAGCCAGAGGGTGAGAGCGCTTCCAGGCGAGTGATGATGACCGGTTCATAGCC 1098  
Db 871 AGCTGGGCGAGATCCACAGAGGCGAGGGGCGCTCTGAGCAGGCGCATGGCCGCGCACAGCC 930

Qy 1099 ACCAGGCGCTTGGGACTAGCCAGTCCCGCAAGTGGTGAAACACAGGTAGATGCCAAGGA 1158  
Db 931 ACTCAGGCGCTTCGCTGGCGCCCGCCCAAGTGGTGATGCCAGGAGATGCG- - - - GA 986

Qy 1159 GGCCAAGTGAGCTGACTCCCGGTTTTTCTTCTCTCCAGCGCCCTTTTGGTCTCTTCTCTGGA 1218  
Db 987 GGCCAAGTGAGCTGAGCCCCAGATTTCTTCCCTTGGATGCTTTCGTTCCCTCCCCAA 1046

Qy 1219 TCTTGTCTTCCAGAGATGGGCTCTGTGGAAGTCTGA- GACTGGGTGTGATGATGGCA 1277  
Db 1047 CCCTTCCCTCGGGCTGGGCTCTGCTGGATTTTGAATTTAGAGTTTGGGGTGTGGCGCATGGCG 1106

Qy 1278 CTAGGCT- - - - ACGGGGCTTCCCGAGTATGTCGCCAGCGCTCTTCTTACCTATGGTG 1333  
Db 1107 CTGGGGTGTGAATGGGCGACCCCGAAGTCTGTCCCCAGGCTCTGCCCTGCGGGGGCAG 1166

Qy 1334 AGGCTCCCTTTTCCCATGCTCGCTGCCACCTCTATGGAACCTGAGGAGGTGTTCAAAAGTG 1393  
Db 1167 TGGCTCCCTCCCTGTTGCTCTTCCGCGCTCTCCCGCCCGCCCGCCGCAAGGCGAG 1226

Qy 1394 GACTTGGGAGCCATCTTCTTCCAGCATCTTGCACGACACATGATGTGTGCTGTCTGT 1453  
Db 1227 GGGGTGCTGGCAGCGCGGCG- - - - -TCAGGGGCTGTCTTCTCTGACGCGCTGTTGTGT 1279

Qy 1454 GCTTTGCTGACTGTGGGTGGTCTGCTGCTGTTGTTGGCCCTTTAGTTCC 1502  
Db 1280 GCTTCGCTGAGTGTGGGTGGTCTGCTGTTGTGTGTCATGTGTCATGGCCTTCC 1328

## RESULT 14

AD28342  
ID AD28342 standard; cdna; 1646 BP.

XX AC AD28342;

DT 29-JAN-2004 (first entry)\*

XX Human KPP cDNA - SEQ ID 53.

kinase; phosphatase; KPP; hepatotropic; antiarteriosclerotic;  
antipruritic; cytostatic; haemostatic; muscular; cerebroprotective;  
nootropic; ophthalmological; anticonvulsant; vasotropic; neuroprotective;  
antiParkinsonian; antiasthmatic; antianaemic; antiasthmatic;  
antidiabetic; antiinflammatory; osteopathic; antiarthritic;  
antirheumatic; dermatological; virucide; antibacterial; fungicide;  
antiparasitic; protozoacide; antihelminthic; antitumor; cardiovascular;  
antiarteriosclerotic; immunosuppressive; cell proliferative; cirrhosis;  
hepatitis; arteriosclerosis; psoriasis; primary thrombocytopenia; cancer;

KW developmental; renal tubular acidosis; Becker's muscular dystrophy;  
KW gonadal dysgenesis; hypothyroidism; seizure; neurological;  
KW Pick's disease; cataract; epilepsy; ischaemic cerebrovascular; stroke;  
KW Alzheimer's; Parkinson's; dementia; autoimmune; inflammatory; AIDS;  
KW allergy; anaemia; asthma; diabetes; mellitus; bronchitis; osteoporosis;  
KW osteoarthritis; rheumatoid arthritis; contact dermatitis; gout;  
KW lipid disorder; cholestasis; Gaucher's; diabetes; atherosclerosis; liver;  
KW viral; bacterial; fungal; parasitic; protozoan; helminthic infection;  
KW trauma; gene therapy; human; ss; gene.

OS Homo sapiens.

XX WO2003080805-A2.

XX 02-OCT-2003.

XX 18-MAR-2003; 2003WO-US008715.

XX 19-MAR-2002; 2002US-0366089P.

PR 29-MAR-2002; 2002US-0369248P.

XX (INCY-) INCYTE CORP.

XX Chien D, Jin P, Hawkins PR, Baughn MR, Becha SD, Chang H;  
PI Ding L, Elliott VS, Emerling BM, Gandhi AR, Gietzen KJ, Griffin JA;  
PI Gururajan R, Hafalia AJA, Ison CH, Kable AE, Khare R, Lee SY;  
PI Lee EA, Lu Y, Marquis JP, Lehn-Mason PM, Ramkumar J, Richardson TW;  
PI Swarnakar A, Tran UK, Chawla NK, Yao MG, Yue H, Bhatia U;  
PI Burrill JD, Lee S, Blake JJ, Ho A, Zheng W;

XX WPI; 2004-011523/01.

DR P-PSDB; ADE28290.

XX New human kinases and phosphatases, and polynucleotides encoding them,  
PT useful for treating, preventing or diagnosing e.g. cell proliferative  
PT disorders, inflammatory, autoimmune, viral, bacterial, parasitic or  
PT fungal diseases.

XX Claim 5; SEQ ID NO 53; 340pp; English.

XX The invention relates to a novel isolated kinase and phosphatase (KPP)  
CC polypeptide. The polypeptide of the invention demonstrates hepatotropic,  
CC antiarteriosclerotic, antipsoriatic, cytostatic, haemostatic, muscular,  
CC cerebroprotective, neurotropic, ophthalmological, anticonvulsant,  
CC vasotonic, neuroprotective, antiparkinsonian, antiasthmatic,  
CC antianaemic, antiasthmatic, antidiabetic, antiinflammatory, osteopathic,  
CC antiarthritic, antirheumatic, dermatological, virucide, antibacterial,  
CC fungicide, antiparasitic, protozoacide, antihelminthic, antigitout,  
CC cardiovascular, antiarteriosclerotic and immunosuppressive activities.  
CC The KPP polypeptides may be useful for diagnosing, treating or preventing  
CC cell proliferative disorders including cirrhosis, hepatitis,  
CC arteriosclerosis, psoriasis, primary thrombocytopenia and cancer,  
CC developmental disorders such as renal tubular acidosis, Becker's muscular  
CC dystrophy, gonadal dysgenesis, hypothyroidism or seizures, neurological  
CC disorders e.g. Pick's disease, cataract, epilepsy, ischaemic  
CC cerebrovascular disease, stroke, Alzheimer's disease, Parkinson's disease  
CC or dementia, autoimmune or inflammatory disorders including AIDS,  
CC allergies, anaemia, asthma, diabetes mellitus, bronchitis, osteoporosis,  
CC osteoarthritis, rheumatoid arthritis, contact dermatitis or gout and  
CC lipid disorders such as cholestasis, Gaucher's disease, diabetes,  
CC atherosclerosis or liver disease, as well as viral, bacterial, fungal,  
CC parasitic, protozoan or helminthic infections and trauma. Furthermore,  
CC the polypeptide may be utilised during gene therapy procedures. The  
CC current sequence is that of the human KPP cDNA of the invention.

XX Sequence 1646 BP; 317 A; 489 C; 508 G; 322 T; 0 U; 10 Other;

Query Match 43.2%; Score 671.6; DB 12; Length 1646;

Best Local Similarity 74.5%; Pred. No. 1.3e-166;

Matches 967; Conservative 0; Mismatches 139; Indels 192; Gaps 2;

QY 101 AGACATGCTGCTCAAGAAACAGACGGAGCATCAGCAGTGTCTATGAGATCCGGGA 160

|||||

Db 216 AACATGCTGCTGCTGAAGAAACACACGGAGGACATCAGCAGCGCTCTACGAGATCCGCGA 275  
QY 161 GAAGCTGGGCTCGGGTGCCTTCTCTGAGGTGATGCTGGCCAGGAAAGGGGCTCTGTCTCA 220  
Db 276 GAGGCTCGGCTCGGGTGCCTTCTCGAGGTGGTCTGGCCACAGAGCGGGGCTCCGACACA 335  
QY 221 TCTTGTGGCCCTCAAGTGCATTTCCCAAGAAAGCACTTCGGGGCAAGAGGCCCTTGGTGG 280  
Db 336 CCTGCTGGCCCTCAAGTGCATTTCCCAAGAAAGGGCCCTCGGGGCAAGAGGCCCTTGGTGG 395  
QY 281 GAATGAGATCGGGTACTTGGCAGAAATCAGCCATCCCAACATTTGGCTCTGGAGGAGCT 340  
Db 396 GAACGAGATCGCAGTGTCTCGGTAGGATCAGTCACTCCCAACATCGTCTCTGGAGGATGT 455  
QY 341 CCATGAGAGTCTTCTCATCTCTACTTGGCCATCGAGCTGGTAAACAGGTGTGAACTGTT 400  
Db 456 CCACGAGAGCCCTTCCCAACCTCTACTTGGCCATCGAACTGGTGAAGGGTGGCGAGCTGTT 515  
QY 401 TGACCGCATCATGAGCGGGGCTCTACACAGAGAAAGACGCCACCTTTGTAGGGCA 460  
Db 516 TGACCGCATCATGAGCGGGGCTCTACACAGAGAAAGGATGCCAGCCATCTGTGGGTCA 575  
QY 461 GGTCTTGGGGCTGTCTCTACCTTCTAGCTGGGCTCGTGCAACGGGACCTCAAGCC 520  
Db 576 GGTCTTGGGGCTGTCTCTACCTTGGGATCGTGCAACGGGACCTCAAGCC 635  
QY 521 TGAAGACCTCTCTATGCCACACCTTTTGGAGACTTCAAGATCATGTCTCTGACTTTGG 580  
Db 636 CGAAGACCTCTCTATGCCACGCCCTTTGAGGACTCGAAGATCATGTCTCTGACTTTGG 695  
QY 581 CTTGTCCAAATACAAGCTGGCAACATGCTAGGCACAGCCCTGTGGGACCCCGAGGATATGT 640  
Db 696 ACTCTCAAAATCCAGGCTGGGAACATGCTAGGCACCGCTGTGGGACCCCTGGATATGT 755  
QY 641 G----- 641  
Db 756 GGTGAGGAGCAGACACCTTGAGGCTTGTCTGGAGTGGGGTGGCCCTGGGGACCCCTAGACA 815  
QY 642 ----- 641  
Db 816 GCGGGGAAGGCTGTGTGGCCGTTGCTTGTGTGGGCATCTCTGGGCTTGATAGGCC 875  
QY 642 ----- 641  
Db 876 GAGCCAGTGACACTGAGCGGCATGGCTGTGTGTGCTGTGTCTGTCTGTCTC 935  
QY 642 -----GCCCGAGAGTCTTGGAGAGAAACCTTACGGGAAGGCGTATGATGTGTGG 692  
Db 936 TGGCCCCCAGCCCCAGAGCTCTTGGAGCAGAAACCTTACGGGAAGGCGTATGATGTGTGG 995  
QY 693 GCCCTGGGTGTCTCTCATCTCTGTGTGGGTACCCCTTCTATGATGAGAGC 752  
Db 996 GCCCTGGGGTGTCTCTCATCTCTGTGTGGGTACCCCTTCTTACGACGAGAGC 1055  
QY 753 GATCCTGAACTCTTTCAGCCAGATTTCTGAGGCGCAGCTATGAGTTTGAATCCCTTTTGG 812  
Db 1056 GACCTGAGCTCTTTCAGCCAGATCTTGGGCGCAGCTATGAGTTTGAATCTCTCTCTCTGG 1115  
QY 813 GATGACATCTCAGAAATCAGCAAGATTTATTCGCACTTCTTGGAAAGCTGATCCCGAG 872  
Db 1116 GATGACATCTCAGAAATCAGCAAGATTTATTCGCGACCTTCTTGGAGCGAGAGACCCCGAG 1175  
QY 873 AAGAGTTTCACTTCCGAGAGGCGCTTACGATCTTTGGATCTCTTGGGATGCGAGCTTC 932  
Db 1176 AAGAGTTTCACTTCCGAGAGGCGCTTGGGACCTTTGGATCTCTTGGGACACAGCTTC 1235  
QY 933 GATAGGAGACATCTCTGGGTCTTGTGAGTGAAGATTTTGGCAGGACCCAGC 992  
Db 1236 GACAGGAGACATCTTAGGCTCTGTGAGCAGATCGGAGAACTTTGTCTCGGACACAC 1295  
QY 993 TGGAGGCGGTGATTCATAGCCACATTCATTCCTAGCTCACATTCGTAAGCTGGGCAAGC 1052  
Db 1296 TGGAGGCGGCTTCAATGCCACCTCTCTCTGGCCACATCCGGAAGCTGGGGCAGATC 1355







Db 538 ACTCTCCAAAATCCAGGCTGGGAACATGCTAGGCACCGCCTGTGGGACCCCTGGATATGT 597  
Qy 641 GGCCCCAGAGCTCTGGAGCAGAAACCTACGGGAAGCCGCTAGATGTGTGGGCCCTGGG 700  
Db 598 GGCCCCAGAGCTCTGGAGCAGAAACCTACGGGAAGCCGCTAGATGTGTGGGCCCTGGG 657  
Qy 701 TGTCAATCTCCACATCTCTGTGTGTGGGTACCCGCCCTTCTATGATGAGAGCGATCCCTGA 760  
Db 658 CGTCATCTCTCCATCTCTGTGTGTGGGTACCCGCCCTTCTACGACGAGAGCGACCCCTGA 717  
Qy 761 ACTCTTCAGCCAGATCTTCAGGGCCAGCTATGATTTGACTCCGCCCTTTTGGGATGACAT 820  
Db 718 GCTCTTCAGCCAGATCTTCAGGGCCAGCTATGATTTGACTCTCTCTTTCTGGGATGACAT 777  
Qy 821 CTCAGATTCAGCCAAAGACTTTCATTCGCCACCTTCTGGAACGTGATCCCCAGAAAGAGTT 880  
Db 778 CTCAGATTCAGCCAAAGACTTTCATTCGCCACCTTCTGAGCGAGACCCCCAGAAAGAGTT 837  
Qy 881 CACCTGCGAGCAGCCCTTACAGCATCTTTTGGATCTCTGGGGATCAGCCTTCGATAGGGA 940  
Db 838 CACCTGCGAACAGGCCCTTGGCGACCTTTGGATCTCTGGGGACACAGCCTTCGACAGGGA 897  
Qy 941 CATCTGGGTTCTGTCACTGAGCAGATCCAGAAATTTTCCAGGACCCACTGGAAGCG 1000  
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Qy 1001 TGCAATTCAGTCCACATCATTTCTACGTCACTCCGTAAGCTGGGACAAAGCCCGAGAGGG 1060  
Db 958 AGCCTTCATGCCACCTCTCTCGGCCACATCCGGNAGCTGGGCGNAGATCCCGAGAGGG 1017  
Qy 1061 TGAGGAGGCTCCAGGCGAGTGTATGACCCGTCAATAGCCACCCAGGCCCTTGGGACTAGCCA 1120  
Db 1018 CGAGGGGCGCTCTGAGCAGGGCATGGCCCGCCACAGCCACTCAGGCCCTCCGCTGTGGCCA 1077  
Qy 1121 GTCCCCCAAGTGTGTAACCAAGGTAGTCCCAAGG 1156  
Db 1078 GCCCCCCAAGTGTGATGTCGCCAGGCAGATGCCGAGG 1113

Search completed: June 6, 2005, 00:35:56  
Job time : 1277 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 5, 2005, 23:59:55 ; Search time 409 Seconds  
(without alignments)  
6217.051 Million cell updates/sec

Title: US-10-032-254A-1  
Perfect score: 1554  
Sequence: 1 gttcgagtcctccactc.....caaaaaaaaaaaaaaaaaa 1554

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA: \*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq: \*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/backfiles.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description        |
|------------|--------|-------------|--------|----|--------------------|
| 1          | 1261.2 | 81.2        | 1458   | 4  | US-09-230-896C-5   |
| 2          | 859    | 55.3        | 1584   | 4  | US-09-799-451-205  |
| 3          | 844.4  | 54.3        | 1282   | 2  | US-08-878-989-12   |
| 4          | 844.4  | 54.3        | 1282   | 3  | US-09-272-796-12   |
| 5          | 844.4  | 54.3        | 1282   | 4  | US-09-016-434-953  |
| 6          | 500.8  | 32.2        | 1442   | 4  | US-09-949-016-1590 |
| 7          | 500.8  | 32.2        | 1442   | 4  | US-09-949-016-1591 |
| 8          | 500.8  | 32.2        | 1480   | 4  | US-09-016-434-1454 |
| 9          | 436.2  | 28.1        | 1074   | 4  | US-09-733-388-3    |
| 10         | 436.2  | 28.1        | 1074   | 4  | US-10-446-175-3    |
| 11         | 436.2  | 28.1        | 1158   | 4  | US-09-733-388-1    |
| 12         | 436.2  | 28.1        | 1158   | 4  | US-10-446-175-1    |
| 13         | 436.2  | 28.1        | 1671   | 4  | US-09-733-388-5    |
| 14         | 436.2  | 28.1        | 1671   | 4  | US-10-446-175-5    |
| 15         | 436.2  | 28.1        | 1733   | 4  | US-09-620-312D-526 |
| 16         | 428.4  | 27.6        | 2447   | 4  | US-09-960-643-1    |
| 17         | 428.2  | 27.6        | 1694   | 4  | US-09-579-664B-3   |
| 18         | 428.2  | 27.6        | 1694   | 4  | US-10-355-975A-3   |
| 19         | 399    | 25.7        | 2165   | 4  | US-09-620-312D-809 |
| 20         | 251.8  | 16.2        | 1503   | 4  | US-09-797-039-3    |
| 21         | 251.8  | 16.2        | 2297   | 4  | US-09-797-039-1    |
| 22         | 251.8  | 16.2        | 2747   | 4  | US-09-620-312D-19  |
| 23         | 251.8  | 16.2        | 2840   | 4  | US-09-620-312D-20  |
| 24         | 251.8  | 16.2        | 3124   | 3  | US-09-734-030-1    |
| 25         | 251.8  | 16.2        | 3124   | 4  | US-10-153-921-1    |
| 26         | 251.8  | 16.2        | 3124   | 4  | US-10-669-689-1    |
| 27         | 218.2  | 14.0        | 781    | 4  | US-09-016-434-851  |

|    |       |      |      |   |                    |                    |
|----|-------|------|------|---|--------------------|--------------------|
| 28 | 217.8 | 14.0 | 3471 | 2 | US-08-715-568A-2   | Sequence 2, Appli  |
| 29 | 196.8 | 12.7 | 2454 | 4 | US-09-992-481-3    | Sequence 3, Appli  |
| 30 | 196.8 | 12.7 | 2454 | 4 | US-10-434-034-3    | Sequence 3, Appli  |
| 31 | 196.8 | 12.7 | 2824 | 4 | US-09-992-481-5    | Sequence 5, Appli  |
| 32 | 196.8 | 12.7 | 2824 | 4 | US-10-434-034-5    | Sequence 5, Appli  |
| 33 | 188   | 12.1 | 2298 | 4 | US-09-975-326-3    | Sequence 3, Appli  |
| 34 | 188   | 12.1 | 2298 | 4 | US-10-217-357-3    | Sequence 3, Appli  |
| 35 | 188   | 12.1 | 2301 | 4 | US-09-975-326-1    | Sequence 1, Appli  |
| 36 | 188   | 12.1 | 2301 | 4 | US-10-217-357-1    | Sequence 1, Appli  |
| 37 | 181.8 | 11.7 | 5703 | 4 | US-09-949-016-673  | Sequence 673, App  |
| 38 | 181.8 | 11.7 | 5703 | 4 | US-09-949-016-4012 | Sequence 4012, Ap  |
| 39 | 181.8 | 11.7 | 5708 | 4 | US-09-566-921-21   | Sequence 21, Appli |
| 40 | 177   | 11.4 | 2218 | 4 | US-09-820-790B-1   | Sequence 1, Appli  |
| 41 | 175.4 | 11.3 | 2061 | 3 | US-09-800-960-1    | Sequence 1, Appli  |
| 42 | 175.4 | 11.3 | 2061 | 4 | US-10-096-960-1    | Sequence 1966, Ap  |
| 43 | 168.6 | 10.8 | 2157 | 4 | US-09-949-016-1966 | Sequence 4, Appli  |
| 44 | 167.6 | 10.8 | 1429 | 2 | US-09-159-385-4    | Sequence 4, Appli  |
| 45 | 167.6 | 10.8 | 1429 | 3 | US-09-186-277-4    | Sequence 4, Appli  |

ALIGNMENTS

RESULT 1  
US-09-230-896C-5  
; Sequence 5, Application US/09230896C  
; Patent No. 6635479  
; GENERAL INFORMATION:  
; APPLICANT: The Scripps Research Institute  
; APPLICANT: Sutcliffe, et al.  
; TITLE OF INVENTION: Hypothalamus-Specific Polypeptides  
; FILE REFERENCE: TSRI-548.1  
; CURRENT APPLICATION NUMBER: US/09/230,896C  
; PRIOR FILING DATE: 1999-02-02  
; PRIOR APPLICATION NUMBER: 60/023,220  
; PRIOR FILING DATE: 1996-08-02  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 1458  
; TYPE: DNA  
; ORGANISM: ratus ratus  
; ORGANISM: ratus ratus  
US-09-230-896C-5

|                       |     |   |               |            |              |
|-----------------------|-----|---|---------------|------------|--------------|
| Query Match           |     | 81.2%   | Score 1261.2; | DB 4;      | Length 1458; |
| Best Local Similarity |     | 93.6%   | Pred. No. 0;  |            |              |
| Matches 1346;         |     | Conservative  | 0;            | Mismatches | 63;          |
|                       |     |   |               | Indels     | 29;          |
|                       |     |   |               | Gaps       | 2;           |
| Qy                    | 99  | GCAGACATGCTGCTGCTCAAGAAACACAGACGAGGACATCAGCAGTGTCTATGAGATCCGG | 158           |            |              |
| Db                    | 44  | GCAGACATGCTGCTGCTCAAGAAACACAGACGAGGACATCAGCAGTGTCTATGAGATCCGG | 103           |            |              |
| Qy                    | 159 | GAGAGCTGGCTCGGTCCTTCTGAGTGTGTCGCCCAAGAAAGGGCTCTGCT            | 218           |            |              |
| Db                    | 104 | GAGAAGCTGGCTCGGTCCTTCTGAGTGTGTCGCCCAAGAAAGGGCTCTGCT           | 163           |            |              |
| Qy                    | 219 | CATCTTGTGCGCTCAAGTGCATTCACAAAGAACACATTCGGGGCAAGAGGCGCTGTG     | 278           |            |              |
| Db                    | 164 | CATCTTGTGCGCTCAAGTGCATTCACAAAGAACACATTCGGGGCAAGAGGCGCTGTG     | 223           |            |              |
| Qy                    | 279 | GAGAATGAGATCGCGGTACTTCGAGAAATCAGCCATCCCAACATTTGGTCTCTGGAGGAC  | 338           |            |              |
| Db                    | 224 | GAGAATGAGATCGCGGTACTTCGAGAAATCAGCCATCCCAACATTTGGTCTCTGGAGGAC  | 283           |            |              |
| Qy                    | 339 | GTCCATGAGAGTCTTCTCATCTCTATGAGAGTGTGTAACAGTGGTGAATG            | 398           |            |              |
| Db                    | 284 | GTCCACGAGAGCCCTTCCCATCTCTATGAGAGTGTGTAACAGTGGTGAATG           | 343           |            |              |
| Qy                    | 399 | TTTGACCGCATGAGAGCGGGCTCTACACAGAGAGGACCGCAGCCACCTTGTAGGG       | 458           |            |              |
| Db                    | 344 | TTTGACCGCATGAGAGCGGGCTCTCTACACAGAGAGGATCGAGCCACTTGTAGGG       | 403           |            |              |
| Qy                    | 459 | CAGTCTTGGCGCTGTCTCTACCTTTCATAGCTGGGCATCGTGACCGGGACCTCAAG      | 518           |            |              |



|    |      |  |      |
|----|------|--|------|
| Qy | 648  | GAGCTCCTGGAGCAGAAACCCCTACGGGAAGGCCCTAGATGTTGGGCCCTGGGTGTGTCATC | 707  |
| Db | 681  | GAGCTCTTGGAGCAGAAACCCCTACGGGAAGGCCCTAGATGTTGGGCCCTGGGGCTCATC   | 740  |
| Qy | 708  | TCCTTACATCCTGCTGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGTAACCTTTC  | 767  |
| Db | 741  | TCCTTACATCCTGCTGTGTGGGTACCCCCCTTCTACGACGAGAGCGACCTTGAGCTCTTC   | 800  |
| Qy | 768  | AGCCAGATTCTGAGGGCCAGCTATGAGTTTGGACTCCCCCTTTTGGGATGACATCTCAGAA  | 827  |
| Db | 801  | AGCCAGATCCTGAGGGCCAGCTATGAGTTTGGACTCTCTTTTCTGGGATGACATCTCAGAA  | 860  |
| Qy | 828  | TCAGCCAAAGACTTCATTCTGGCCACTTCTTGAAAGTGATCCCAAGAGAGGTTCACTGC    | 887  |
| Db | 861  | TCAGCCAAAGACTTCATTCTGGCCACTTCTTGAGCGGAGACCCCAAGAGAGGTTCACTGC   | 920  |
| Qy | 888  | CAGCAGGCCCTACAGCATCTTTGGATCTCTGGGGATGCAGCCTTTCGATAGGGAATCCTG   | 947  |
| Db | 921  | CAACAGGCCCTTGGGCACTTTGGATCTCTGGGGACACAGCCTTTCGACAGGGAATCTTA    | 980  |
| Qy | 948  | GGTTCTCTCAGTGAGCAGATCCAGAAATTTTCCAGGACCCACTGGAAAGCTGCATTC      | 1007 |
| Db | 981  | GGCTCTCTCAGTGAGCAGATCCGAAAGACTTTGCTCGGACACTGGAGCGAGCCTTC       | 1040 |
| Qy | 1008 | AATGCCACATCTTCTTACGTCACATCCGTAAGCTGGGACAAAGCCACAGAGGTTGAGGAG   | 1067 |
| Db | 1041 | AATGCCACCTCGTTCTCTCGGCCACATCCGGAAGCTGGGGCAGATCCACAGAGGGCGAGGG  | 1100 |
| Qy | 1068 | GCCTCAGGCAGGTGATGACCGGTATAGCACCCAGGCCCTTGGGACTAGGCAGTCCGCC     | 1127 |
| Db | 1101 | GCCTCTGAGCAGGGCATTGGCCGCGCACAGCCACTCAGGCCCTCCGTGTGGCCAGCCGCC   | 1160 |
| Qy | 1128 | AAGTGTGTAAAAACAGGTAGATGCCAAGGAAGGCCAAGTGGACACTCCCGGTTTTTCT     | 1187 |
| Db | 1161 | AAGTGTGTATGCCAGGCAGATGCC----GAGGCCAAGTGGACTGACCCCCAGATTTCCCT   | 1216 |
| Qy | 1188 | TTCTCTCAGGCCCTTTTGGTCTCTTTCTTGATCCTTGTCTCCAGACTGGCCTCTGCTGG    | 1247 |
| Db | 1217 | TCCTCTTGATGCTTTCCGTCCCTCCCAACCCCTCCCTCTGGGCTGGCCTCTGCTGG       | 1276 |
| Qy | 1248 | AAAGTCTGA-GACTGGGTGTGATGATGGCACTAGGTT----ACGGGGCTTTCCCACTAT    | 1302 |
| Db | 1277 | ATTTTGAGATTTGAGGGTGTGGCGCATGGCGCTGGGGTTGGAATGGGGCACCCCAAGTC    | 1336 |
| Qy | 1303 | GTCCCCCAGCCTCTATTCTTACCTATGGTGGAGGCTCCCTTTCCCATGTGCTGCCACCC    | 1362 |
| Db | 1337 | TGTCCTCCAGGCTCTGCCCTGCCTGGGGGCACTGGCTCCCTCTCCCTCTTGCTCTCCGCG   | 1396 |
| Qy | 1363 | TCTATGAAACTGAGGAGGTGTTCAAAGTGGACTCTGGGAGCCATCCTTCTGTGCACCTTG   | 1422 |
| Db | 1397 | CCCTGCCCCCCCCCGCCCAAGCGAGGGGGTGTCTGCAGCGGGGCC-----TC           | 1449 |
| Qy | 1423 | CACGAACACATGCAATTGTGGCTGTCTGTGCTTTGTGCTGACTGTGGTGGTCTGCTTG     | 1482 |
| Db | 1450 | AGGGCTGTCTTCTCTGACGGCTGTGTGTGCTTCCCTGANGTGTGGTGTGCTGCTTG       | 1509 |
| Qy | 1483 | TGTTGTGGCCCTTTAGTTCCTCC-----TTTTTCCTAACCAATAAGACAAACAG         | 1531 |
| Db | 1510 | TGTCATGGTCATGGCCTTCCAGCCCCCTCCAGTGTTCCTCCCAACCAATAAGAAAGATAC   | 1569 |
| Qy | 1532 | AACCAAAAAAAAAA   | 1546 |
| Db | 1570 | AGCAAAAAAAAAAA   | 1584 |

RESULT 3

US-08-878-989-12  
; Sequence 12, Application US/08878989  
; Patent No. 5885803  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Hillman, Jennifer L.

```
QY 461 GGTCTTGGCGCTGTCTCTACCTTATAGCCTGGGCGATCGTGACCGGACCTCAAGCC 520
Db 557 GGTCTTGGCGCGCTGTCTCTACCTTATAGCAGCTGGGATCGTGACCGGACCTCAAGCC 616
QY 521 TGAAGACCTCTCTATGCCACACCTTTTGAAGACTCCAAGATCATGTCTCTGACTTTGG 580
Db 617 CGAAACCTCTGTATGCCACGCGCTTTGAGGACTCGAAGATCATGTCTCTGACTTTGG 676
QY 581 CCTGTCCAAATACAAGCTGGCAACATGCTAGGCACAGCCTGTGGGACCCAGGATATGT 640
Db 677 ACTCTCCAAATACAGGCTGGCAACATGCTAGGCACAGCCTGTGGGACCCCTGGATATGT 736
QY 641 GGCCCGACAGCTCTGAGAGCAGAAACCTTAGGGAAGCCGCTAGATGTGTGGCCCTGGG 700
Db 737 GGCCCGACAGCTCTGAGAGCAGAAACCTTAGGGAAGCCGCTAGATGTGTGGCCCTGGG 796
QY 701 TGTCACTCTACATCTGCTGTGTGGGTACCCCGCTTCTATGATGAGAGCGATCTGA 760
Db 797 CGTCATCTCTACATCTGCTGTGTGGGTACCCCGCTTCTAGCAGAGAGCGACCTGA 856
QY 761 ACTCTTCAGCCAGATCTGAGGCGCAGCTATGAGTTTGACTCCCGCTTTTGGATGACAT 820
Db 857 GCTCTTCAGCCAGATCTGAGGCGCAGCTATGAGTTTGACTNTCTTTCTGGGATGACAT 916
QY 821 CTCAGATCAGCCAAAGACTTTCATTCGCCACCTTCTCGAAACGCTGATCCCGAGAGGTT 880
Db 917 CTCAGATCAGCCAAAGACTTTCATTCGCCACCTTCTCGAGCGAGACCTTCAGAAGAGTT 976
QY 881 CACTGCCACAGCCCTCAGAGATCTTGTGATCTCTGGGATGCGACCTTCGATAGGA 940
Db 977 CACTGCCACAGCCCTTGGGACCTTGTGATCTTTGGGACACAGGCTTTGGCAGGA 1036
QY 941 CATCTCGGTTCTGTAGTGAGCAGATCCAGAAATTTTGCAGGACCCACTTGGAGCG 1000
Db 1037 CATCTTAGGTTGTGATGAGCAGATCCGGAAGACTTTGCTTGGACACACTTGAAGCG 1096
QY 1001 TGAATTCATGCGACATCTTCCTACGTCATCCGTAAGCTGGGACAAAGCCAGAGGG 1060
Db 1097 AGCCTTCAATGCCACCTTGTCTCGCCACATCCGGAAGCTGGGCGAGATCCCGAGGG 1156
QY 1061 TGAGGAGGCTCCAGGCGAGTGTATGACCGTATGACCCAGCCAGGCTTGGAGTACCA 1120
Db 1157 CGAGGGGCTCTGAGCAGGCGATGGSCGNCACAGCACATNAGGCTTCTGCTGGCCA 1216
QY 1121 GTCCCCCAAGTGTGAAAAACAGGTAGATGCCAAGGAAGGCCAAGTGGACTGACTCCCGG 1180
Db 1217 GCCCCCAAGTGTGTGATGTCGCCAGGNAGATGCC----GAGGCCAAGTGGANTGANCCTCAG 1272
QY 1181 TTTTCTTTTC 1190
Db 1273 ATTNTCTNC 1282
```

## RESULT 4

US-09-272-796-12

; Sequence 12, Application US/09272796

; Patent No. 6207148

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Corley, Neil C.

; APPLICANT: Guegler, Karl G.

; APPLICANT: Lal, Preeti

; APPLICANT: Goli, Surya K.

; APPLICANT: Shah, Purvi

; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN

; NUMBER OF INVENTIONS: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

```
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/09/272,796
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/878,989
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1282 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PROSNOT06
; CLONE: 827431
; US-09-272-796-12
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Query Match 54.3%; Score 844.4; DB 3; Length 1282;

Best Local Similarity 86.2%; Pred. No. 2.7e-248;

Matches 940; Conservative 1; Mismatches 145; Indels 4; Gaps 1;

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QY 101 AGACATGCTGCTCTCTCAAGAAACAGACGAGGAGCATCAGCAGTGTCTATGAGATCCGGGA 160
Db 197 AAACATGCTGCTCTCAAGAAACACACGAGGAGCATCAGCAGCGTCTTACGAGATCCGCGA 256
QY 161 GAAGCTGGGCTCGGTCCTTCTCTGAGGTGATGCTGGCCCGAAGAGGGCTCTGTCTCA 220
Db 257 GAGGCTCGGTCGCGTCTTCTCCAGAGTGTGTCTGGCCAGAGCGGGCTCCGCACA 316
QY 221 TCTTTGGCCCTCAAGTGCATTTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTTGGTGA 280
Db 317 CCTGTGGCCCTCAAGTGCATTTCCCAAGAAAGGCCCTTCGGGGCAAGGAGGCCCTTGGTGA 376
QY 281 GAATGAGATCGCGTACTTCGCGAGATCAGCCATGCCAATTTGTGGCTCTGGAGGACGT 340
Db 377 GAACGAGATCGCAGTGTCTCGTAGGATCAGTCAACCCCAACATCGTCTCTGGAGGATGT 436
QY 341 CCATGAGATGCTTCTCTCATCTTCTGTCATGGAGCTGTTACAGTGGTGAACCTTT 400
Db 437 CCACGAGAGCCCTTCCACCTCTTACCTGGCCATGGAACTGTGTACGGGTGGCAGCTGT 496
QY 401 TGACCGCATCATGAGCGGGGCTCTTACACAGAGAAGAGCCAGCCACCTTTGTAGGGCA 460
Db 497 TGACCGCATCATGAGCGGGGCTCTTACACAGAGAAGAGTGCACCATCTGTGGGTCA 556
QY 461 GGTCTTGGCGTGTCTCTTACCTTATAGCTGGGATCGTGCACCGGACCTCAAGCC 520
Db 557 GGTCTTGGCGCGTCTCTTACCTTATAGCTGGGATCGTGCACCGGACCTCAAGCC 616
QY 521 TGAAGACCTCTCTATGCCACACCTTTTGAAGACTCCAAGATCATGTCTCTGACTTTGG 580
Db 617 CGAAACCTCTGTATGCCACGCGCTTTGAGGACTCGAAGATCATGTCTCTGACTTTGG 676
QY 581 CCTGTCCAAATACAAGCTGGCAACATGCTAGGCACAGCCTTGGGACCCAGGATATGT 640
Db 677 ACTCTCCAAATACAGGCTGGCAACATGCTAGGCACAGCCTTGGGACCCCTGGATATGT 736
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|    |      |  |      |
|----|------|--|------|
| Qy | 641  | GGCCCCAGAGCTCTCTGAGAGCAAAACCTTACGGGAAGCCGTAGATGTGTGGGCCCTGGG       | 700  |
| Db | 737  | GGCCCCAGAGCTCTTGTGAGCAGAAACCTTACGGGAAGCCGTAGATGTGTGGGCCCTGGG       | 796  |
| Qy | 701  | TGTCATCTCTACATCTGCTGTGTGGTACCCCCCTTCTATGATCAGAGCGATCTCTGA          | 760  |
| Db | 797  | CGTCATCTCTACATCTGCTGTGTGGTACCCCCCTTCTACAGCAGAGCGACCTCTGA           | 856  |
| Qy | 761  | ACTCTTCAGCCAGATCTCTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACAT      | 820  |
| Db | 857  | GCTCTTCAGCCAGATCTCTGAGGGCCAGCTATGAGTTTGACTTCTTCTGGGATGACAT         | 916  |
| Qy | 821  | CTCAGAAATCAGCCAAAGACTTCATTCCGCCACTTCTCGAAACGTGATCCCCAGAGAGGTT      | 880  |
| Db | 917  | CTCAGAAATCAGCCAAAGACTTATTTCGCCACCTTCTCGAGCGAGACCTTCTCAGAGAGGTT     | 976  |
| Qy | 881  | CACCTGCCAGAGGCCCTTACAGCATCTTTTGGATCTCTGGGGATCGACGCTTCGATAGGGA      | 940  |
| Db | 977  | CACCTGCCAAGCCCTTGCGGACCTTTGGATCTTTTGGGACACAGGCTTTGGCAGGGA          | 1036 |
| Qy | 941  | CATCTCTGGTTCGTCTAGTGAGCAGATCCAGAAGAAATTTTGCACAGGACCCACTGGGAAGCG    | 1000 |
| Db | 1037 | CATCTTAGGGTTGTCTAGTGAGCAGATCCCGAAGAACTTTGCTTTGGACACACTGTGGAAGCG    | 1096 |
| Qy | 1001 | TGCATTCAAATGCCACATCATTTCTACCTGCATCCGTAAGCTGGGACAAAGCCACAGAGG       | 1060 |
| Db | 1097 | AGCCTTCAATGCCACCTTGTTCTTCGCCCCACATCCGGAAGCTGGGGCAGATCCACAGAGG      | 1156 |
| Qy | 1061 | TGAGGAGGCTTCAGGCAGTGATGAGCCCGTCTATAGCCATAGCCACCCAGGCTCTGGGACTAGCCA | 1120 |
| Db | 1157 | CGAGGGGGCTCTGAGCAGGGCATGGSCGNCACAGCCACTNAGGCCCTTGTGCTGGCCA         | 1216 |
| Qy | 1121 | GTCCCCCAAGTGTGAAAAACAGGTAGATGCCAAGGAAGGCCAAAGTGGACTCTCCCGG         | 1180 |
| Db | 1217 | GGCCCCCAAGTGTGTGATGCCAGGNAGATGCC----GAGGCCAAGTGTGANTGANTCCCGAG     | 1272 |
| Qy | 1181 | TTTTTCTTTC   | 1190 |
| Db | 1273 | ATTTCCTTNC   | 1282 |

## RESULT 5

US-09-016-434-953  
; Sequence 953, Application US/09016434  
; Patent No. 6500938  
; GENERAL INFORMATION:  
; APPLICANT: Janice Au-Young  
; APPLICANT: Jeffrey J. Sellhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1490  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/016,434  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:

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QY 881 CACCTGCCAGCGCCCTACAGCATCTTTGGATCTCTGGGATGCGAGCTTCGATAGGA 940
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 977 CACCTGCCAACAGCGCTTGGGACCTTTGGATCTTTTGGGACACAGGCTTTGGCAGGA 1036
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 941 CATCTGGGTTCTGTAGTGAGCAGATCCAGAAAGATTTTGGCAGGACCCACTGGAAGCG 1000
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1037 CATCTAGGTTGTAGTGAGCAGATCCGGAAGACTTGTCTGGACACACTGGAAGCG 1096
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1001 TGCATTCAATGCCACATCATCTTCTAGCTCATCTCCGTAAGCTGGGACAAAGCCAGAGGG 1060
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1097 AGCTTTCAATGCCACCTTTCTCTGGCCACATCCGGAAGCTGGGCGAGATCCAGAGGG 1156
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1061 TGAGGAGGCTCCAGGAGTGATGACCCGTCTATAGCCACCCAGGCTTGGACTAGCCA 1120
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1157 CGAGGGGGCTCTGAGCAGGCGCATGGSCCGNCACAGCCACTNAGGCTTCTGTCTGGCCA 1216
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1121 GTCCCCCAAGTGTGAAACCCAGCTAGATGCCAAGGAAGCCAAAGTGAGCTCCCGG 1180
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1217 GCCCCCAAGTGTGATGTCGCCAGGNAGTGCC----GAGGCCAAGTGGANTGANCCCCAG 1272
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1181 TTTTCTTTC 1190
Db ||||| |||||
QY 1273 ATTNCTNC 1282
Db ||||| |||||

RESULT 6
US-09-949-016-1590
; Sequence 1590, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1590
; LENGTH: 1442
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1590

Query Match 32.2%; Score 500.8; DB 4; Length 1442;
Best Local Similarity 72.0%; Pred. No. 8.3e-143;
Matches 668; Conservative 0; Mismatches 257; Indels 3; Gaps 1;

QY 119 GAACAGACGGAGACATCAGCAGTGTCTATGATCCGGAGAGCTGGGCTCGGTGC 178
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 167 GAAGCGCGGAGACATTAAGACATCTACGACTTCCGAGATGTTCTGGGCGACGGGGC 226
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 179 CTTCCTGAGTGATGTGGCCAGGAAAGGGGCTCTGCTCATCTTGTGGCCCTCAAGTG 238
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 227 CTTCCTGAGTGATCTTCGACAGATATAGAGACGACAGAGCTGTGGCCATCAATG 286
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 239 CATTCCCAAGAAACATTTGGGGCAAGGAGGCCCTGTGGAGAAATGAGATTCGGGTACT 298
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 287 CATTGCCAAGAGGCCCTTGGGGCAAGGAGGAGCATGGAGAAATGAGATTTGTCTCT 346
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 299 TCGAGATCAGCATCCCAACATTTGGCTCTCGGAGAGCTCCATCAGAGTCTTCTCA 358
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 347 GCAAGATCAAGACCCCAACATTTAGCCCTGGATGACATCTATGAGAGTGGGGCCA 406
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 359 TCTTACTTGGCCATGAGCTGGTAACAGAGTGTGTGAACCTGTGACCGCATCATGAGCG 418
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 407 CCTTACCTCATCATGAGCTGGTGTCCGGTGGGAGCTCTTTGACCGTATTTGTGAAA 466
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
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QY 419 GGGCTCCTACACAGAGAAGGACGCCAGCCACCTTTAGGGCAGGTCTTTGGCGCTGTCTC 478
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 467 AGGCTTTCTACAGGAGCGGACGCCAGCCGCTCATCTTCCAGTGTGGATGCTGTGAA 526
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 479 CTACCTTTATAGCTCGGCGATCGTCAACGGGACCTCAAGCCTGAAACCTCTCTATGC 538
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 527 ATACCTGCAATGACCTGGGATGTACACCGGATCTCAAGCCAGAGATCTGCTGTACTA 586
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 539 CACACCTTTTGGAGACTCCAAGATCATGTCTCTGACTTTTGGCTGTCTCAAAATACAA- 597
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 587 CAGCCTGGATGAAGACTTCCAAATCATGATCTCCGACTTTTGGCTCTTCCAAAGTGGAG 646
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 598 --CTGCAACATGCTAGGACAGCCCTGTGGGACCCAGGATATGTGGCCCCAGAGCTCCT 655
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 647 CCGGCGCATGTGCTCTCCACCGCTGTGGAACCTCCGGGATACGTGGCCCCCTGAAGTCT 706
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 656 GGAGCAGAAACCTTACGGGAAGCCGTAGATGTGTGGGCCCTGGGTGTCTATCTCTACAT 715
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 707 GGGCCAGAGCCCTACAGCAGGCTGTGATTTGCTTCCATAGTGTCTATCGCTACAT 766
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 716 CTTGCTGTGGGTACCCCCCTTTCTATGATGAGAGCGATCTTGAACTCTTCAGCCAGAT 775
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 767 CTTGCTCTGGGTTACCTCTCTATGACGAGAATGATGCCAAACTCTTTGAAACAGAT 826
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 776 TCTGAGGGCCAGCTATGAGTTGACTTCCCTTTTGGATGACATCTCAGAAACAGCAA 835
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 827 TTTGAAGGGCGGAGTACGAGTTTGAATCTCTTACTGGGAGCATCTCTGACTCTGCCAA 886
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 836 AGACTTTCATTGCGCACCTTCTGAAAGCTGATCCCCAGAGAGGTTTCACTGCCAGCAGGC 895
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 887 AGATTTTCATCCGCACTTGTATGAGAGAGGACCCAGAGAAAGATTTCACCTGTGAGCAGGC 946
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 896 CTTACAGCATCTTTTGGATCTCTGGGATGACGCTTCGATAGGAGACATCTCTGGGTCTGT 955
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 947 CTTGACGACCCCATGGATTGACGAGATACAGCTCTAGATAAGAAATATCCACCAGTCGT 1006
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 956 CAGTGAGCAGATCCAGAGAAATTTTCCAGGACCCACTGGAAGGCTGATTCATTCAGTCCAC 1015
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1007 GAGTGAGCAGATCAAGAAGAACTTTGCCAAGAGCAAGTGGAAAGCAAGCCTTCAATGCCAC 1066
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1016 ATCATTTCTTACGTACATCCGTAAGCTG 1043
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1067 GGCTGTGTGCGGCACATGAGGAAACTG 1094
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
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## RESULT 7

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US-09-949-016-1591
; Sequence 1591, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1591
; LENGTH: 1442
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1591

Query Match 32.2%; Score 500.8; DB 4; Length 1442;
Best Local Similarity 72.0%; Pred. No. 8.3e-143;
```



| Matches | 668; | Conservative   | 0;  | Mismatches | 257; | Indels | 3; | Gaps | 1; |
|---------|------|--|---|------------|------|--------|----|------|----|
| Qy      | 119  | GA   | AACAGACGAGGAGACATCAGCAGTGTCTATAGATCCGGGAGAAAGCTGGGCTCGGGTGC | 178        |      |        |    |      |    |
| Db      | 167  | GA   | AGCAGCGGAGGACATTAAGAGACATCTACGACTTCCGAGATGTTCTGGGACAGGGGGC  | 226        |      |        |    |      |    |
| Qy      | 179  | CTTCTCTGAGGTGATGCTGGCCAGGAAAGGGGCTCTGCTCATCTTGTGGCCCTCAAGTG    | 238   |            |      |        |    |      |    |
| Db      | 227  | CTTCTCGGAGGTGATCTCGGAGAAGATATAGAGGACGAGAGCTGTGTGGCCATCAAAATG   | 286   |            |      |        |    |      |    |
| Qy      | 239  | CAITTTCCCAAGAAAGCACATTCGGGCAAGGAGGCCCTCGTGAGGAATGAGATCGCGGTACT | 298   |            |      |        |    |      |    |
| Db      | 287  | CAITTTCCCAAGAGGCCCTTGGAGGCAAGGAAGCGAGCATGGAGNAATGAGATGCTGTCTCT | 346   |            |      |        |    |      |    |
| Qy      | 299  | TGGCAGAAATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTTCATGAGAGTCTCTTCTCA | 358   |            |      |        |    |      |    |
| Db      | 347  | GCACAAGATCAAGCACCCCAACATTGTAGCCCTGATGACATCTATGAGAGTGGGGGCCA    | 406   |            |      |        |    |      |    |
| Qy      | 359  | TCCTCTACTTGGCCATGAGCTGGTAAACAGGTGGTGAACCTGTTTGACCGCATCATGGAGCG | 418   |            |      |        |    |      |    |
| Db      | 407  | CTCTCTACTCATCATGACGTGGTGTGGGTGGGAGCTCTTTGACCGTATTTGTGAAAA      | 466   |            |      |        |    |      |    |
| Qy      | 419  | GGGCTCTACACAGAGAAGGACGCCGCCACCTTGTAGGGCAGGTCTTGGCGCTGTCTC      | 478   |            |      |        |    |      |    |
| Db      | 467  | AGGCTTCTACACGGAGCGGAGCGCCAGCGCTCATCTTCCAGGTGCTGGATGCTGTGAA     | 526   |            |      |        |    |      |    |
| Qy      | 479  | CTACCTTCATAGCTTGGCATTCGTGCAACGGGACCTCAAGCCTGAAAAACCTCTCTATGC   | 538   |            |      |        |    |      |    |
| Db      | 527  | ATACCTGCATGACCTGGGCATTTGACACCGGATCTCAAGCCAGAGAATCTGCTGTACTA    | 586   |            |      |        |    |      |    |
| Qy      | 539  | CACACCTTTTGGAGACTCCAAGATCATGGTCTCTGACTTTTGGCTGTGCCAAATACAAAG-  | 597   |            |      |        |    |      |    |
| Db      | 587  | CAGCTTGGATGAAGACTTCAAAATCATGATCTCCGACTTTGGCTCTTCCAAAGATGGAGGA  | 646   |            |      |        |    |      |    |
| Qy      | 598  | --CTGGCAACATGCTAGGCACAGCCTCTGGGACCCAGGATATGTGGCCCCAGAGCTCTCT   | 655   |            |      |        |    |      |    |
| Db      | 647  | CCCGGCGAGTGTCTCTCCACCGCTGTGGAACTCCGGGATACGTGGCCCTGAACTCT       | 706   |            |      |        |    |      |    |
| Qy      | 656  | GGAGCAAAACCTTACGGGAAGCCGTAGATGTGTGGGCCCTGGGTGTCTATCTCTACAT     | 715   |            |      |        |    |      |    |
| Db      | 707  | GGCCCAAGCCCTTACAGCAAGGTGTGTGATTTGCTGTCTCATAGTGTCTATCGCTACAT    | 766   |            |      |        |    |      |    |
| Qy      | 716  | CTGTCTGTGTGGTATACCCCTCTTATGATGAGAGCATCTTGAACTCTTCAGCCAGAT      | 775   |            |      |        |    |      |    |
| Db      | 767  | CTTGCTCTGGTTTACCCTCCCTTCTATGAGGAATGTGCCAACTCTTTGAAACAGAT       | 826   |            |      |        |    |      |    |
| Qy      | 776  | TCTGAGGCCAGCTATGAGTTTGACTCCCTCTTTGGGATGACATCTCAGAAATCAGCCAA    | 835   |            |      |        |    |      |    |
| Db      | 827  | TTTGAAGCCGAGTACGAGTTTGACTCTCTCTTACTGGGACGACATCTCTGACTCTGCCAA   | 886   |            |      |        |    |      |    |
| Qy      | 836  | AGACTTCATTTCGCCACCTTCTGGAAACGTGATCCCCAGAGAGGTTTCACTTGCACGAGGC  | 895   |            |      |        |    |      |    |
| Db      | 887  | AGATTTTTCATCCGGCATTGTATGGAGAAGGACCCAGAGAAAAGTTCACCTGTGTAGCAGGC | 946   |            |      |        |    |      |    |
| Qy      | 896  | CCTACAGCATTTTGGATCTCTGGGATGAGCCTTCGATAGGAGACATCTGGGTCTGT       | 955   |            |      |        |    |      |    |
| Db      | 947  | CTTGACGACCCCATGGATTGAGGAGATACAGCTCTTAGTAAGAAATATCCACCACTCGGT   | 1006  |            |      |        |    |      |    |
| Qy      | 956  | CAGTGACAGATCCAGAAGAATTTTGGCAGGACCCACTGGAAGCGTGCATTTCAATGCCAC   | 1015  |            |      |        |    |      |    |
| Db      | 1007 | GAGTGACAGATCAAGAAGAACTTTGCCNAGAGCAAGTGGNAGCAAGCCTTCAATGCCAC    | 1066  |            |      |        |    |      |    |
| Qy      | 1016 | ATCATCTCTAGTCAATTCGGTAAGCTG                                    | 1043  |            |      |        |    |      |    |
| Db      | 1067 | GGCTGTGGTGGCAGCATGAGAACTG                                      | 1094  |            |      |        |    |      |    |

## RESULT 8

RESOL 8  
US-09-016-434-1454

US-09-016-434-1434  
; Sequence 1454, Application US/09016434

; Sequence 1334, App.  
; Patent No. 6500938

FACEBOOK NO. 8300938  
GENERAL INFORMATION:

APPLICANT: Janice Au-Young

QY 539 CACACCTTTTGAGGACTCCAAAGATCATGCTCTGACTTTGGGCTGTCCAAATACAAG- 597  
DB 597 CAGCTGGATGAAGACTCCAAATCATGATCTCGACTTTGGGCTCTCCAAAGATGAGGA 656  
QY 598 --CTGGCAACATGCTAGGCACAGCTGTGGGACCCAGAGATATGTGGCCCCAGAGCTCCT 655  
DB 657 CCGGGCAGTGTGCTCTCCACCGCTGTGGAATCTCCGGGATAGTGGCCCTGAAATCCT 716  
QY 656 GGAGCAGAAACCTTACGGGAAGCCGTPAGATGTGTGGGCCCTGGGTGTCTATCTCTTACAT 715  
DB 717 GGCCCAAGAGCCCTACAGCAAGCTGTGGATTTGCTGTCTCATAGGTGTCTATGCTTACAT 776  
QY 716 CTTGCTGTGTGGGTACCCCTCTTATATGATGAGAGGATCTTGAATCTTTACAGCAGAT 775  
DB 777 CTTGCTGTGGGTGTACCTCTCTTATGACGAGATGATGCCAAATCTTTGAACAGAT 836  
QY 776 TCTGAGGGCCAGCTATGAGTTTGAATCTTCACTCCCTTTTGGGATGACATCTCAGAATCAGCAA 835  
DB 837 TTTGAAGGCCAGTACAGAGTTTGAATCTTCACTCTTCTTACTGGGACGACATCTCTGACTTGC 896  
QY 836 AGACTTTCATTCGACACCTCTCTGAAACGTGATCCCCAGAGAGGTTTCACTTGCAGCAGGC 895  
DB 897 AGATTTCATCCGCACTTGTGAGAGAGGCCAGAGAGATTCACCTGTGAGCAGGC 956  
QY 896 CTTACAGCATCTTTGGATCTCTGGGATGAGCCTTTCGATAGGACATCTCTGGGTCTGT 955  
DB 957 CTTGCAACCCATGATTCAGGAGATACAGCTCTAGATAAGAAATATCCACCAGTGGT 1016  
QY 956 CAGTGAGCAGATCCAGAGAAATTTGCCAGAGCCCTGGAAGGCTGCAATTCATTCAGTCCAC 1015  
DB 1017 GAGTGAGCAGATCAAGAAGAACTTTGCCAGAGCAAGTGGAAAGCAAGCCCTTCAATGCCAC 1076  
QY 1016 ATCATTCCTACGTACATCCGTAACTG 1043  
DB 1077 GGCTGTGGTGGGACATGAGAACTG 1104

## RESULT 9

## US-09-733-388-3

; Sequence 3, Application US/09733388

; Patent No. 6602698

; GENERAL INFORMATION:

; APPLICANT: Donoho, Greg

; APPLICANT: Scoville, John

; APPLICANT: Turner, C. Alexander Jr.

; APPLICANT: Friedrich, Glenn

; APPLICANT: Zambrowicz, Brian

; APPLICANT: Abuin, Alejandro

; APPLICANT: Sands, Arthur T.

; TITLE OF INVENTION: No. 6602698el Human Kinase Proteins and

; FILE OF INVENTION: Polynucleotides Encoding the Same

; FILE REFERENCE: LEX-0103-USA

; CURRENT APPLICATION NUMBER: US/09/733,388

; CURRENT FILING DATE: 2000-12-07

; PRIOR APPLICATION NUMBER: US 60/169,428

; PRIOR FILING DATE: 1999-12-07

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 1074

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-733-388-3

Query Match 28.1%; Score 436.2; DB 4; Length 1074;

Best Local Similarity 67.6%; Pred. No. 4.6e-123;

Matches 628; Conservative 0; Mismatches 298; Indels 3; Gaps 1;

QY 117 AAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAGCTGGGCTCGGGT 176

DB 37 AAAAAGCAAGCTGAAGACATCAAGAGATCTTCGAGTTCAAAGAGACCTTCGGAACCGGG 96

QY 177 GCCTTCTCTGAGTGATGCTGGCCAGGAAAGGGCTCTCTCATCTTGTGGCCCTCAAG 236  
DB 97 GCCTTTTCCGAAGTGTGTTTAGCTGAAGAGAAGCAACTGGCAAGCTCTTTGCTGTGAAG 156  
QY 237 TGCATTCCCAAGAACACACTTCGGGGCAAGGAGGCCCTTGGTGAGAAATGAGATGCGGTA 296  
DB 157 TGTATCCCTAAGAAAGCGCTGAAGGCAAGGAAAGCAGCATAGAGAATGAGATAGCGGTC 216  
QY 297 CTTGCGAGAAATCAGCCATCCAAACATTTGGGCTCTGGAGGACGTCATGAGAGTCTTCT 356  
DB 217 CTGAGAAAGATTAAAGCATGAAAAATATTGTTGCCCTGGAAGACATTTATGAAGCCCAAT 276  
QY 357 CATCTCTACTTGGCCATGGAGCTGTAACAGAGTGTGAACCTGTTTGAACCCCATCATCGAG 416  
DB 277 CACTGTACTTGTGTCAATGAGCTGGTGTCCGGTGGAGAGCTGTTTGAACCCGATAGTGAG 336  
QY 417 CGGGGCTCTTACACAGAGAAGGACGCCAGCACCTTGTATGGGAGAGTCTTTGGCGCTGTG 476  
DB 337 AAGGGGTTTATACAGAGAAGGATGCCAGCACTCTGATCCGCAAGTCTTTGGACGCCGTG 396  
QY 477 TCCTACTTCATAGCCTGGGCAATCGTGCAACGGGACCTCAAGCCTGAAAACCTCTCTAT 536  
DB 397 TACTATCTCCACAGAAATGGGCATCGTCCACAGAGACCTCAAGCCCGAAAAATCTCTGTAC 456  
QY 537 GCCACACCTTTTGAGGACTCCAAAGATCATGCTCTGACCTTTGGCCTGTCCAAATACAA 596  
DB 457 TACAGTCAAGATGAGGAGTCCAAATAATATGATCAGTGACTTTGGATTGTCAAATAATGAG 516  
QY 597 G---CTGGCAACATGCTAGGCACAGAGCTGTGGGACCCAGGATATGTGGCCCAAGAGTGC 653  
DB 517 GGCAAGGAGATGTGATGTCCACTGCTGTGGAACTCCAGGCTATGTCTCTGAAAGTC 576  
QY 654 CTGGAGCAGAAACCTTACGGGAAGGCGGTAGATGTGTGGGCCCTTGGGTGTCTCTCTAC 713  
DB 577 CTGCGCCAGAAACCTTACAGCAAAAGCGTTGACTGTCTGTGTCATCGGAGTGAATGCTCTAC 636  
QY 714 ATCTCTGTGTGGGTACCCCTTCTATGATGAGAGCGATCCTGAACCTTTCAGGCCAG 773  
DB 637 ATCTTGTCTGTGGGCTACCCCTCTTTTATGATGAAATGACTCCAAGCTCTTTGAGCAG 696  
QY 774 ATTCTGAGGCCAGCTATGATGATTTGACTCCCTCTTTTGGGATGACATCTCAGAAATCAGCC 833  
DB 697 ATCTCNAAGGCGGAATATGATTTGACTCTCTCTCTACTTGGGATGACATCTCCGACTCTGCA 756  
QY 834 AAGACTTCAATTCGCACCTCTCTGGAACGTGATCCCAAGAGAGTTTCACTGCCAGCAG 893  
DB 757 AAGAGCTTCAATTCGGAACCTTGTATGGAGAGGACCCGAAATAAAGATACACGTTGTGAGCAG 816  
QY 894 GCCTTACAGCATCTTTGGATCTCTGGGGATGCGCCCTTCGATAGGGACATCTCTGGGTCT 953  
DB 817 GCAGCTCGGCACCCATGGATCGGTGGTGACACAGCCCTCAACAAAAACATCCAGAGTCC 876  
QY 954 GTCAGTGAGCAGATCCAGAAAGAAATTTTCCAGGAGCCCACTGGAAAGCGGTGCAATTCATGCCC 1013  
DB 877 GTACGCGCCAGATCCGGAAGAACTTTTGCCAGAGCAAAATGGAGACAAAGCATTTAATGCC 936  
QY 1014 ACATCATCTCTACGTACATCCGTAACT 1042  
DB 937 ACGGCGCTGTGAGACATATGAGAAAACT 965

## RESULT 10

## US-10-446-175-3

; Sequence 3, Application US/10446175

; Patent No. 6806073

; GENERAL INFORMATION:

; APPLICANT: Donoho, Greg

; APPLICANT: Scoville, John

; APPLICANT: Turner, C. Alexander Jr.

; APPLICANT: Friedrich, Glenn

; APPLICANT: Zambrowicz, Brian

; APPLICANT: Abuin, Alejandro

; APPLICANT: Sands, Arthur T.

; TITLE OF INVENTION: No. 6806073el Human Kinase Proteins and  
; FILE REFERENCE: Lex-0103-USA  
; CURRENT APPLICATION NUMBER: US/10/446,175  
; CURRENT FILING DATE: 2003-05-27  
; PRIOR APPLICATION NUMBER: US/09/733,388  
; PRIOR FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: US 60/169,428  
; PRIOR FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3

; LENGTH: 1074  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-446-175-3

Query Match 28.1%; Score 436.2; DB 4; Length 1074;

Best Local Similarity 67.6%; Pred. No. 4.6e-123;

Matches 628; Conservative 0; Mismatches 298; Indels 3; Gaps 1;

```
Qy 117 AAGAAACAGACGAGGACATCAGCAGTCTCTATGAGATCCGGGAGAGCTGGGCTCGGGT 176
Db 37 AAAAGCAAGCTGAAGACATCAAGAATCTTCGAGITCAAAGAGACCCTCGGAACCGG 96
Qy 177 GCCTTCTCTGAGGTGATCTGCGCCAGGAAAGGGGCTCTGCTCATCTTTGTGGCCCTCAAG 236
Db 97 GCCTTTTCGAGTGTGTTAGCTGAAGAGAGCACTGGCAAGCTCTTGTCTGTAAG 156
Qy 237 TGCATTTCCAAAGAAAGCACTTCGGGGCAAGAGAGCCCTGGTGGAGATGAGATCGCGGTA 296
Db 157 TGTATCCCTAAGAGAGCGCTGAAGGGCAAGGAAAGCAGCATAGAGATGAGATAGCCGTC 216
Qy 297 CTTGCGAATCAGCCATCCCAACATTTGCTCTGGAGGAGCTCCATGAGAGTCTTCT 356
Db 217 CTGAGAAAGATTAAGCATGAAATATTGTGCCCTGGAAGACATTTATGAAGGCCAAAT 276
Qy 357 CATCTCTACTTTGGCCATGAGCTGGTAACAGTGGTGAATCTTTGACCGCATCATGGAG 416
Db 277 CACCTGTACTTGTTCATGACCTGGTGTCCGGTGGAGAGCTGTTGACCGGATAGTGAG 336
Qy 417 CGGGGCTCCTACACAGAGAGAGCCAGCCACCTTTGAGGCGAGTCTTTGGCGCTGTC 476
Db 337 AAGGGGTTTTATACAGAGAGAGATGCCAGCACTCTGATCCGCCAAGTCTTGGAGCCGTC 396
Qy 477 TCCTACCTTCATAGCTGGCATCGTGCAACGGGACCTCAAGCTTGAAACCTCTCTAT 536
Db 397 TACTATCTCCACAGATGGGCATCGTCCACAGAGACCTCAAGCCCGAAATCTCTTTGAC 456
Qy 537 GCCACACCTTTTGAGGACTCCAAAGATCATGGTCTCTGACTTTGGGCTCTCCAAATACAA 596
Db 457 TACAGTCAAGATGAGAGTCCAAATATATGATCAGTGACTTTGGATTGTCAAATAGAG 516
Qy 597 G---CTGGCAATCTAGGACACAGCTGTGGGACCCAGGATATGTGGCCCGCCAGAGCTC 653
Db 517 GCGAAAGAGATGTGATGTCCACTGCTGTGGAACTCCAGGCTATGTGCTCTCTGAAGTC 576
Qy 654 CTGGAGGAGAAACCTTACGGAAGCCCGTATGATGTGGGCGCTGGGCTGATCTCTTAC 713
Db 577 CTGCGCCAGAAACCTTACAGCAAGCCGTTGACTGTGCTGGTCCATCGGAGTGAITGGCTTAC 636
Qy 714 ATCTGTCTGTGGGTACCCCTTCTATGATGAGAGCGATCTCTGACTCTTCAGCCAG 773
Db 637 ATCTTGTCTGTGGGTACCCCTTCTTATGATGAATATGATCTCAAGCTCTTTGAGCG 696
Qy 774 ATCTGAGGCGCAGCTATGAGTTTGACTCCCGCTTTTGGGATGACATCTCAGAAATCAGCC 833
Db 697 ATCTCAAGGCGGAATATGAGTTTGACTCTCCCTACTGGATGACATCTCCGACTCTGCA 756
Qy 834 AAAGACTTCATTGCGCACTTCTGGAACGTCGATCCCGAGAGAGGTTCACTCGCCAGAG 893
Db 757 AAAGACTTCATTGCGAACCCTGATGGAAGAGGAGCCGGAATAAAGATACACGTTGTGAGCAG 916
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Qy 894 GCCCTACAGCATCTTTGGATCTCTGGGATGACAGCCTTCGATAGGAGACATCTCGGTTCT 953
Db 817 GCAGCTCGGCACCATCATGATCGCTGGTGACACAGCCCTCAACAAACATCCACGAGTCC 876
Qy 954 GTGAGTGAAGAGATCCAGAGAAATTTTGCAGGAGCCACTGGAAGCGTGCATTCATGCCC 1013
Db 877 GTGAGCGCCAGATCCCGGAAACCTTTGCGCAAGAGCAATGAGAGCAAGCATTTAATGCC 936
Qy 1014 ACATCATCTCTACGTACATCCCGTAAGCT 1042
Db 937 ACGGCCGTCGTGAGACATATGAGAAACT 965
```

#### RESULT 11

US-09-733-388-1

; Sequence 1, Application US/09733388

; Patent No. 6602698

; GENERAL INFORMATION:

; APPLICANT: Donoho, Greg

; APPLICANT: Scoville, John

; APPLICANT: Turner, C. Alexander Jr.

; APPLICANT: Friedrich, Glenn

; APPLICANT: Zambrowicz, Brian

; APPLICANT: Abuin, Alejandro

; APPLICANT: Sands, Arthur T.

; TITLE OF INVENTION: No. 6602698el Human Kinase Proteins and

; FILE REFERENCE: Lex-0103-USA

; CURRENT APPLICATION NUMBER: US/09/733,388

; CURRENT FILING DATE: 2000-12-07

; PRIOR APPLICATION NUMBER: US 60/169,428

; PRIOR FILING DATE: 1999-12-07

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 1158

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-733-388-1

Query Match

Best Local Similarity 67.6%; Pred. No. 4.8e-123;

Matches 628; Conservative 0; Mismatches 298; Indels 3; Gaps 1;

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Qy 117 AAGAAACAGACGAGGACATCAGCAGTCTCTATGAGATCCGGGAGAGCTGGGCTCGGGT 176
Db 37 AAAAGCAAGCTGAAGACATCAAGAATCTTCGAGITCAAAGAGACCCTCGGAACCGG 96
Qy 177 GCCTTCTCTGAGGTGATCTGCGCCAGGAAAGGGGCTCTGCTCATCTTTGTGGCCCTCAAG 236
Db 97 GCCTTTTCGAGTGTGTTAGCTGAAGAGAGCACTGGCAAGCTCTTGTCTGTAAG 156
Qy 237 TGCATTTCCAAAGAAAGCACTTCGGGGCAAGAGAGCCCTGGTGGAGATGAGATCGCGGTA 296
Db 157 TGTATCCCTAAGAGAGCGCTGAAGGGCAAGGAAAGCAGCATAGAGATGAGATAGCCGTC 216
Qy 297 CTTGCGAATCAGCCATCCCAACATTTGCTCTGGAGGAGCTCCATGAGAGTCTTCT 356
Db 217 CTGAGAAAGATTAAGCATGAAATATTGTGCCCTGGAAGACATTTATGAAGGCCAAAT 276
Qy 357 CATCTCTACTTTGGCCATGAGCTGGTAACAGTGGTGAATCTTTGACCGCATCATGGAG 416
Db 277 CACCTGTACTTGTTCATGACCTGGTGTCCGGTGGAGAGCTGTTGACCGGATAGTGAG 336
Qy 417 CGGGGCTCCTACACAGAGAGAGGAGCCAGCCACTTGTAGGGCAGGCTCTTGGCGCTGTC 476
Db 337 AAGGGGTTTTATACAGAGAGAGATGCCAGCACTCTGATCCGCCAAGTCTTGGAGCCGTC 396
Qy 477 TCCTACCTTCATAGCTGGGCATCGTGCAACGGGACCTCAAGCTTGAAACCTCTCTAT 536
Db 397 TACTATCTCCACAGATGGGCATCGTCCACAGAGACCTCAAGCCCGAAATCTCTTTGAC 456
Qy 537 GCCACACCTTTTGAGGACTCCAAAGATCATGGTCTCTGACTTTGGGCTCTCCAAATACAA 596
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Db 457 TACAGTCAAGATGAGGAGTCCAAATATATGATCAGTGACTTTGGATTGTCAAAATGGAG 516
Qy 597 G---CTGGCAACATGCTAGGACAGACCTGTGGGACCCAGGATATGTGGCCCCAGAGCTC 653
Db 517 GGCAAAGGAGATGTGATGTCCACTGCTGTGGAACTCCAGGCTATGTGCGTCTCTGAAGTC 576
Qy 654 CTGGAGCAGAAACCTCAGCGGAAGCGGTAGATGTGTGGGCCCTGGGTGTCATCTCTCTAC 713
Db 577 CTGCCCCAGAAACCTTACAGCAAGCGGTTGACTGCTGTGTCCTATCGGAGTGTGCTCTAC 636
Qy 714 ATCCTGCTGTGGTACCCCTCTTATGATGAGAGCGATCCTGAACCTCTTTCAGCCAG 773
Db 637 ATCTTGCTCTGCGGCTACCTCTCTTTTATGATGAATAATGATCTCCAGACTTTTGGAGCAG 696
Qy 774 ATTCTGAGGCCAGCTATGAGTTGATCTCCCTCTTTTGGGATGACATCTCAGAATCAGCC 833
Db 697 ATCTCAAGCGGAATATGAGTTTGAATCTCTCTCTGAGTACATCTCCGACTCTGCA 756
Qy 834 AAAGACTTCAATTCGCCACCTCTTGGAAAGCTGATCCCGAAGAGGTTTACCTGCGAGCAG 893
Db 757 AAAGACTTCAATTCGCCACCTCTTGGAAAGCTGATCCCGAAGAGGTTTACCTGCGAGCAG 816
Qy 894 GCCTACAGCATCTTTGAGTCTCTGGGATGACGCTTTCATAGGAGACATCTCTGGGTCT 953
Db 817 GCAGCTCGGACCATGGATGCTGTGTGACAGCCCTCAACAAACATCCAGAGTCC 876
Qy 954 GTCAGTGAGCAGATCCAGAAAGATTTTGGCAGGACCCACTGGAGCGTGTCAATTCAATGCC 1013
Db 877 GTCAGGCCCAGATCCGGAATACTTTGGCCAGAGCAAAATGGAGCAACGATTTAATGCC 936
Qy 1014 ACATCATCTCTACGTCACTCCGTAAGCT 1042
Db 937 ACGGCCGCTGTGAGACATATGAGAAAAC 965
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## RESULT 12

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US-10-446-175-1
; Sequence 1, Application US/10446175
; Patent No. 6806073
; GENERAL INFORMATION:
; APPLICANT: Donoho, Greg
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Abuin, Alejandro
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6806073el Human Kinase Proteins and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/10/446,175
; PRIOR FILING DATE: 2003-05-27
; PRIOR FILING DATE: US/09/733,388
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,428
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1158
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-446-175-1
Query Match 28.1%; Score 436.2; DB 4; Length 1158;
Best Local Similarity 67.6%; Pred. No. 4.8e-123;
Matches 628; Conservative 0; Mismatches 298; Indels 3; Gaps 1;
```

```
Qy 117 AAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAAGCTGGGCTCGGGT 176
Db 37 AAAAAAGCAAGCTGAAGACATCAAGAGATCTTCGAGTTCAAAGAGACCTTCGGAACCGGG 96
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Qy 177 GCCTTCTCTGAGTGATGCTGGCCAGGAAAGGGCTCTGCTCATCTTGTGGCCCTCAAG 236
Db 97 GCCTTTTTCGAAGTGTGTTTAGCTGAAGAGAAAGCAACTGGCAAGCTCTTTCGTGTGAAG 156
Qy 237 TGCATTTCCCAAGAAACACTTTCGGGGCAAGGAGGCCCTTGGTGAGAAATGAGATCGCGGTA 296
Db 157 TGTATCCCTAAAGAGCGCTGAAGGGCAAGGAAAGCAGCATAGAGAATGAGATGAGCGGTC 216
Qy 297 CTTTCGAGAAATCAGCCATCCCAACATTTGTGGCTCTGAGGAGACGTCCATGAGAGTCTTCT 356
Db 217 CTGAGAAAGATTAAGCATGAAAATATTTGTTCCTCGAAGACATTTATGAAGCCCAAAAT 276
Qy 357 CATCTCTACTTGGCCATGAGCTGTGTAACAGGTGGTGAACCTTTGTGACCCCATCATCGAG 416
Db 277 CACCTGTACTTGTGTATGAGCTGTGTCGCTGGAGAGCTGTTTGAACCGGATAGTGAG 336
Qy 417 CGGGGCTCTCTACACAGAGAAAGGACGCCAGCACCTTTGTAGGGCAGGTCCTTGGCGGTGTC 476
Db 337 AAGGGGTTTTATACAGAGAAAGGATGCCAGCACTCTGATCCGCAAGTCTTTGGAGCGCGTG 396
Qy 477 TCCTACTTCTATGAGCTGTGGCATCTGTGCAACGGGACCTCAAGCTTGAAAACCTCTCTAT 536
Db 397 TACTATCTCCACAGAAATGGGCATCGTCCACAGAGACCTCAAGCCCGAAAATCTCTGTGAC 456
Qy 537 GCCACACCTTTTTCAGGACTCCAAAGATCATGCTCTGACTTTTGGCCTGTCCAAATACAA 596
Db 457 TACAGTCAAGATGAGGAGTCCAAAATATATGATCAGTGACTTTGGATTGTCAAAATGGAG 516
Qy 597 G---CTGGCAACATGCTAGGCAAGCTGTGGGACCCAGGATATGTGGCCCCAGAGCTC 653
Db 517 GGCAAAGGAGATGTGATGTCCACTGCTGTGGAACTCCAGGCTATGTGCGTCTCTGAAAGTC 576
Qy 654 CTGGAGCAGAAACCTTACGGGAAGCGGTAGATGTGTGGGCCCTTGGGTGTCATCTCTAC 713
Db 577 CTGCCCCAGAAACCTTACAGCAAGCGGTTGACTGCTGTGTCCTCATCGGAGTGAITGCGCTAC 636
Qy 714 ATCTGCTGTGTGGGTACCCCTCTTATGATGAGAGCGATCCTGAACCTCTTCAGCCAG 773
Db 637 ATCTTGTCTGTGGGCTACCTCTCTTTTATGATGAATAATGACTCCAAGCTCTTTTGAGCAG 696
Qy 774 ATTCTGAGGCCAGCTATGAGTTTGAATCTCCCTCTTTTGGGATGACATCTCAGAAATCAGCC 833
Db 697 ATCTCAAGCGGAATATGAGTTTGAATCTCTCTCTACTTGGGATGACATCTCCGACTCTGCA 756
Qy 834 AAAGACTTCAATTCGCCACCTCTTGGAAAGCTGATCCCGAAGAGGTTTACCTGCGAGCAG 893
Db 757 AAAGACTTCAATTCGCCACCTCTGATGGAGAGGACCCGAAATAAAGATACACGTTGTGAGCAG 816
Qy 894 GCCTACAGCATCTTTGAGTCTCTGGGATGACGCTTTCATAGGAGACATCTCTGGGTCT 953
Db 817 GCAGCTCGGACCATGGATGCTGTGTGACAGCCCTCAACAAACATCCAGAGTCC 876
Qy 954 GTCAGTGAGCAGATCCAGAAAGATTTTGGCAGGACCCACTGGAGCGTGTCAATTCAATGCC 1013
Db 877 GTCAGGCCCAGATCCGGAATACTTTGGCCAGAGCAAAATGGAGCAACGATTTAATGCC 936
Qy 1014 ACATCATCTCTACGTCACTCCGTAAGCT 1042
Db 937 ACGGCCGCTGTGAGACATATGAGAAAAC 965
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## RESULT 13

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US-09-733-388-5
; Sequence 5, Application US/09733388
; Patent No. 6602698
; GENERAL INFORMATION:
; APPLICANT: Donoho, Greg
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Abuin, Alejandro
; APPLICANT: Sands, Arthur T.
```

```
; TITLE OF INVENTION: No. 6602698el Human Kinase Proteins and
; FILE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0103-USA
; CURRENT APPLICATION NUMBER: US/09/733,388
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,428
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1671
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-733-388-5

Query Match      28.1%; Score 436.2; DB 4; Length 1671;
Best Local Similarity 67.6%; Pred. No. 6.1e-123;
Matches 628; Conservative 0; Mismatches 298; Indels 3; Gaps 1;

QY 117 AAGAAACAGACGAGGACATCAGCAGTGTCTATGAGATCCGGAGAAAGCTGGGCTCGGGT 176
DB 117 AAGAAACAGACGAGGACATCAGCAGTGTCTATGAGATCCGGAGAAAGCTGGGCTCGGGT 176
QY 203 AAAAAAGCAAGCTGAAGACATCAAGAAAGATCTTCGAGTTCAAAGAGACCCCTCGGAACCGG 262
DB 203 AAAAAAGCAAGCTGAAGACATCAAGAAAGATCTTCGAGTTCAAAGAGACCCCTCGGAACCGG 262
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DB 177 GCCTTCTCTGAGGTGATGCTGGCCAGGAAAGGGGCTCTGCTCATCTTTGGCCCTCAAG 236
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DB 237 TGCATTTCCTCAAGAAAGCACTTCGGGCAAGGAGGCGCTCGTGAGAAATCAGATCGCGGTA 296
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DB 323 TGTATCCCTTAAGAGGCGCTGAAGGCAAGGAAAGCAGCATAGAGAAATCAGATAGCGGTC 382
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DB 443 CACCTGTACTTGGTCTATGAGCTGGTGTCCGGTGGAGAGCTGTTTGACCGGATAGTGGAG 502
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DB 563 TACTATCTCCAGAAATGGGCATCTGTCACAGAGACCTCAAGCCCGAAATCTCTTTGTAC 622
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DB 537 GCCACACCTTTTGAGGACTCCAAGATCATGCTCTGACTTTTGGCGCTGTCCAAATACAA 596
QY 623 TCAGTCAAGATGAGGAGTCCAAATATATGATCAGTGACTTTGGATTTGCAAAATGGAG 682
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DB 597 G---CTGGCAACATGCTAGGCAAGCAGCTGTGGGACCCAGGATATGTGGCCCGCAGAGCTC 653
QY 683 GGCAGAGGAGATGTGATGTCCTACTGCTGTGGAATCTCAGGCTATGCTCGCTCTGAAGTC 742
DB 683 GGCAGAGGAGATGTGATGTCCTACTGCTGTGGAATCTCAGGCTATGCTCGCTCTGAAGTC 742
QY 654 CTGGAGCAGAAACCTTACGGAAGGCGGTAGATGTGTGGGCCCTGGGTGTCTCTAT 713
DB 654 CTGGAGCAGAAACCTTACGGAAGGCGGTAGATGTGTGGGCCCTGGGTGTCTCTAT 713
QY 743 CTGGCCAGAAACCTTACAGCAAGCGGTGACTGTGCTGCTCCATCGGAGTGTGCTCTAC 802
DB 743 CTGGCCAGAAACCTTACAGCAAGCGGTGACTGTGCTGCTCCATCGGAGTGTGCTCTAC 802
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DB 714 ATCCTGCTGTGGGTACCCCTCTCTATGATGAGCGGATCCTGAACTCTTCAGCCAG 773
QY 803 ATCTTCTCTGGGCTACCCCTCTCTTTTATGATGAAATGACTCCAAAGCTTTTGGAGCAG 862
DB 803 ATCTTCTCTGGGCTACCCCTCTCTTTTATGATGAAATGACTCCAAAGCTTTTGGAGCAG 862
QY 774 ATCTGAGGGCCAGCTATGAGTTGACTCCCTCTTTTGGATGACATCTCAGAAATCAGGC 833
DB 774 ATCTGAGGGCCAGCTATGAGTTGACTCCCTCTTTTGGATGACATCTCAGAAATCAGGC 833
QY 863 ATCTCAGGGCGAATATGAGTTTGAATCTCTCCCTACTGGGATGACATCTCCGACTCTGCA 922
DB 863 ATCTCAGGGCGAATATGAGTTTGAATCTCTCCCTACTGGGATGACATCTCCGACTCTGCA 922
QY 834 AAGACTTCTATTCGCCACCTTCTGGAAAGCTGTATCCCGAGAGAGGTTTCACTGCCAGCAG 893
DB 834 AAGACTTCTATTCGCCACCTTCTGGAAAGCTGTATCCCGAGAGAGGTTTCACTGCCAGCAG 893
QY 923 AAGACTTCTATTCGGAACTCTGTGGAGAGGAGGCCGAAATAAAGATATACACGTGTGAGCAG 982
DB 923 AAGACTTCTATTCGGAACTCTGTGGAGAGGAGGCCGAAATAAAGATATACACGTGTGAGCAG 982
QY 894 GCCTTACAGATCTTTGGATCTCTGGGGATGAGCCCTTCGATAGGAGACATCTCTGGGTTCT 953
DB 894 GCCTTACAGATCTTTGGATCTCTGGGGATGAGCCCTTCGATAGGAGACATCTCTGGGTTCT 953
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## RESULT 14

US-10-446-175-5

; Sequence 5, Application US/10446175

; Patent No. 6806073

; GENERAL INFORMATION:

; APPLICANT: Donoho, Greg

; APPLICANT: Scoville, John

; APPLICANT: Turner, C. Alexander Jr.

; APPLICANT: Friedrich, Glenn

; APPLICANT: Zambrowicz, Brian

; APPLICANT: Abuin, Alejandro

; APPLICANT: Sands, Arthur T.

; TITLE OF INVENTION: No. 6806073el Human Kinase Proteins and

; FILE OF INVENTION: Polynucleotides Encoding the Same

; FILE REFERENCE: LEX-0103-USA

; CURRENT APPLICATION NUMBER: US/10/446,175

; CURRENT FILING DATE: 2003-05-27

; PRIOR APPLICATION NUMBER: US/09/733,388

; PRIOR FILING DATE: 2000-12-07

; PRIOR APPLICATION NUMBER: US 60/169,428

; PRIOR FILING DATE: 1999-12-07

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5

; LENGTH: 1671

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-446-175-5

Query Match

28.1%; Score 436.2; DB 4; Length 1671;

Best Local Similarity 67.6%; Pred. No. 6.1e-123;

Matches 628; Conservative 0; Mismatches 298; Indels 3; Gaps 1;

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Db 623 TACAGTCAGATGAGGAGTCCAAATAATGATCAGTGACTTTGGATTGTCAAAATGGAG 682
QY 597 G---CTGGCAACATGCTAGGCAAGCCTGTGGACCCCAAGGATATGTGGCCCAAGAGTTC 653
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QY 654 CTGGAGCAGAACCCCTACGGGAGGCGGTAGATGTGTGGCCCTGGGTGTCATCTCCTAC 713
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QY 1014 ACATCATCTCTACGTACATCCGTAGCT 1042
Db 1103 ACGGCGCTGTGAGACATATGAGAAAAC 1131
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## RESULT 15

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US-09-620-312D-526
; Sequence 526, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunding
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pc_FL_genes Version 1.0
; SEQ ID NO 526
; LENGTH: 1733
; TYPE: DNA
; ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (215)..(1372)
US-09-620-312D-526
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Query Match 28.1%; Score 436.2; DB 4; Length 1733;
Best Local Similarity 67.6%; Pred. No. 6.2e-123;
Matches 628; Conservative 0; Mismatches 298; Indels 3; Gaps 1;
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

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(without alignments)  
1396.855 Million cell updates/sec

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22: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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| 2          | 903.8  | 58.2  | 1452  | 17     | US-10-425-114-26649 | Sequence 26649, A |
| 3          | 859    | 55.3  | 1584  | 17     | US-10-302-172-205   | Sequence 205, App |
| 4          | 844.4  | 54.3  | 1282  | 10     | US-09-769-970-12    | Sequence 12, Appl |
| 5          | 844.4  | 54.3  | 1282  | 17     | US-10-305-720-953   | Sequence 953, App |
| 6          | 844.4  | 54.3  | 1282  | 18     | US-10-656-598-5     | Sequence 5, Appli |
| 7          | 844.4  | 54.3  | 1282  | 18     | US-10-643-795A-9    | Sequence 9, Appli |
| 8          | 844.4  | 54.3  | 1282  | 19     | US-10-948-518-9     | Sequence 9, Appli |
| 9          | 544    | 35.0  | 641   | 18     | US-10-656-598-15    | Sequence 15, Appl |
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| 11         | 500.8  | 32.2  | 1480  | 17     | US-10-305-720-1454  | Sequence 1454, Ap |

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| 14 | 436.2 | 28.1 | 1074 | 14 | US-10-024-036B-3    | Sequence 3, Appli  |
| 15 | 436.2 | 28.1 | 1074 | 17 | US-10-446-175-3     | Sequence 3, Appli  |
| 16 | 436.2 | 28.1 | 1074 | 18 | US-10-782-695-34    | Sequence 34, Appli |
| 17 | 436.2 | 28.1 | 1074 | 19 | US-10-936-445-3     | Sequence 3, Appli  |
| 18 | 436.2 | 28.1 | 1158 | 10 | US-09-733-388-1     | Sequence 1, Appli  |
| 19 | 436.2 | 28.1 | 1158 | 17 | US-10-446-175-1     | Sequence 1, Appli  |
| 20 | 436.2 | 28.1 | 1158 | 19 | US-10-936-445-1     | Sequence 1, Appli  |
| 21 | 436.2 | 28.1 | 1578 | 9  | US-09-835-788A-6    | Sequence 6, Appli  |
| 22 | 436.2 | 28.1 | 1578 | 16 | US-10-175-042-6     | Sequence 6, Appli  |
| 23 | 436.2 | 28.1 | 1579 | 18 | US-10-737-450-1     | Sequence 1, Appli  |
| 24 | 436.2 | 28.1 | 1661 | 17 | US-10-258-106-29    | Sequence 29, Appli |
| 25 | 436.2 | 28.1 | 1671 | 10 | US-09-733-388-5     | Sequence 5, Appli  |
| 26 | 436.2 | 28.1 | 1671 | 17 | US-10-446-175-5     | Sequence 5, Appli  |
| 27 | 436.2 | 28.1 | 1671 | 19 | US-10-936-445-5     | Sequence 5, Appli  |
| 28 | 436.2 | 28.1 | 1733 | 15 | US-10-037-270-526   | Sequence 526, App  |
| 29 | 436.2 | 28.1 | 1733 | 17 | US-10-117-722-526   | Sequence 526, App  |
| 30 | 436.2 | 28.1 | 1736 | 17 | US-10-258-106-20    | Sequence 20, Appl  |
| 31 | 436.2 | 28.1 | 1772 | 14 | US-10-024-036B-1    | Sequence 1, Appli  |
| 32 | 436.2 | 28.1 | 1772 | 18 | US-10-782-695-32    | Sequence 32, Appl  |
| 33 | 436.2 | 28.1 | 2235 | 19 | US-10-887-553A-1018 | Sequence 1018, Ap  |
| 34 | 431.2 | 27.7 | 709  | 11 | US-09-764-875-128   | Sequence 128, App  |
| 35 | 430   | 27.7 | 1383 | 10 | US-09-935-464-2     | Sequence 2, Appli  |
| 36 | 430   | 27.7 | 1383 | 14 | US-10-125-835-2     | Sequence 2, Appli  |
| 37 | 430   | 27.7 | 1738 | 10 | US-09-935-464-4     | Sequence 4, Appli  |
| 38 | 430   | 27.7 | 1738 | 14 | US-10-125-835-4     | Sequence 4, Appli  |
| 39 | 428.4 | 27.6 | 2447 | 9  | US-09-960-643-1     | Sequence 1, Appli  |
| 40 | 428.4 | 27.6 | 2447 | 17 | US-10-380-235-3     | Sequence 3, Appli  |
| 41 | 428.2 | 27.6 | 1694 | 16 | US-10-355-975-3     | Sequence 3, Appli  |
| 42 | 409   | 26.3 | 981  | 16 | US-10-090-002-1     | Sequence 1, Appli  |
| 43 | 409   | 26.3 | 981  | 18 | US-10-740-835-2     | Sequence 2, Appli  |
| 44 | 409   | 26.3 | 1372 | 9  | US-09-817-181-1     | Sequence 1, Appli  |
| 45 | 409   | 26.3 | 1372 | 14 | US-10-300-828-1     | Sequence 1, Appli  |

## ALIGNMENTS

## RESULT 1

US-09-735-138-5  
; Sequence 5, Application US/09735138  
; Publication No. US20030176666A1

## GENERAL INFORMATION:

APPLICANT: Sutcliffe, J. Gregor  
Gautvik, Kaare M.  
De Lecea, Luis  
Bloom, Floyd E.  
Danielson, Patria E.  
Kilduff, T.S.  
Gautvik, Vigdis T.  
Foye, Pamela E.

TITLE OF INVENTION: Hypothalamus-Specific Polypeptides

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Olson & Hierl, Ltd.

STREET: 20 No. US20030176666A1th Wacker Drive, 36th Floor

CITY: Chicago

STATE: IL

COUNTRY: USA

ZIP: 60606

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/735,138

FILING DATE: 12-Dec-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/023,220

FILING DATE: 02-AUG-1996

ATTORNEY/AGENT INFORMATION:  
; NAME: Talivaldis Cepuritis  
; REGISTRATION NUMBER: 20,818  
; REFERENCE/DOCKET NUMBER: TSRI 548.1 DIV.1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-580-1180  
; TELEFAX: 312-580-1189  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1458 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-735-138-5

Query Match 81.2%; Score 1261.2; DB 10; Length 1458;  
Best Local Similarity 93.6%; Pred. No. 0;  
Matches 1348; Conservative 0; Mismatches 63; Indels 29; Gaps 2;

QY 99 GCAGACATGCTGCTCAAGAAACAGACGAGGACATCAGCAGTGCTATGAGATCCGG 158  
DB 44 GCAGACATGCTGCTCAAGAAACAGACGAGGACATCAGCAGTGCTATGAGATCCGG 103  
QY 159 GAGAAGCTGGGCTCGGCTCTCTGAGGTGATGCTGGCCCGAGAAAGGGCTCTGCT 218  
DB 104 GAGAAGCTGGGCTCGGCTCTCTGAGGTGATGCTGGCCCGAGAAAGGGCTCTGCT 163  
QY 219 CATCTTGTGGCCCTCAAGTGATTCACAAAGACATTCGGGGCAAGAGGCGCTGGTG 278  
DB 164 CATCTTGTGGCCCTCAAGTGATTCACAAAGACATTCGGGGCAAGAGGCGCTGGTG 223  
QY 279 GAGAAAGAGATCGGCTGCTTCCAGAAACAGACATTCAGGATTCGGCTCTGGAGGAC 338  
DB 224 GAGAAAGAGATCGGCTGCTTCCAGAAACAGACATTCAGGATTCGGCTCTGGAGGAC 283  
QY 339 GTCCATGAGAGTCTCTCATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAAGTG 398  
DB 284 GTCCATGAGAGTCTCTCATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAAGTG 343  
QY 399 TTTGACCGCATATGAGCGGGCTCTCTACAGAGAAAGCGCAGCCACCTGTAGGG 458  
DB 344 TTTGACCGCATATGAGCGGGCTCTCTACAGAGAAAGCGCAGCCACCTGTAGGG 403  
QY 459 CAGGTCTTGGCGCTGCTCTACCTCATAGCTGGGATCGTGACCGGACCTCAAG 518  
DB 404 CAGGTCTTGGCGCTGCTCTACCTCATAGCTGGGATCGTGACCGGACCTCAAG 463  
QY 519 CCTGAAACCTCTCTATGACACACCTTTTGGAGACTTCCAGATCATGGTCTCTGACTTT 578  
DB 464 CCTGAAACCTCTCTATGCCACACCTTTTGGAGACTTCCAGATCATGGTCTCTGACTTT 523  
QY 579 GGCTGTCCAAATACAAAGCTGGCAATGCTAGGACAGCCCTGTGGACCCCAAGATAT 638  
DB 524 GGCTGTCCAAATATCAAGCTGGCAATGCTAGGACAGCCCTGTGGACCCCAAGATAT 583  
QY 639 GTGGCCCCAGAGTCTCTGGAGCAGAAACCTTACGGGAAGCCGTAGATGTGGGCCCTG 698  
DB 584 GTGGCCCCAGAGTCTCTGGAGCAGAAACCTTACGGGAAGCCGTAGATGTGGGCCCTG 643  
QY 699 GGTGTCTATCTCTACATCTCTGCTGTGGGTACCCCCCTTCTATGATGAGAGCATCTCT 758  
DB 644 GGTGTCTATCTCTACATCTCTGCTGTGGGTACCCCCCTTCTATGATGAGAGCATCTCT 703  
QY 759 GAACCTTTGAGCCAGATCTGAGGCGCAGCTATGAGTTTGACTCCCTTTTGGGATGAC 818  
DB 704 GAACCTTTGAGCCAGATCTGAGGCGCAGCTATGAGTTTGACTCTCCCTTTTGGGATGAC 763  
QY 819 ATCTCAGAAATCAGCCAAAGACTTCATTCTGGCCACCTTCTGGAACGTGTATCCCGAGAGG 878

Db 764 ATCTCAGAAATCAGCCAAAGACTTCATTCTGGCACCTTCTGGAACGTGTATCCCGAGAGG 823  
QY 879 TTACCTTCCAGCAGGCGCTTACAGCATCTTTGGATCTCTGGGATGAGCCTTTCGATAGG 938  
Db 824 TTACCTTCCAGCAGGCGCTTACAGCATCTCTGGATCTCTGGGATGAGCCTTTCGATAGG 883  
QY 939 GACATCTGGGTTCTGTAGTGAGCAGATCCAGAAATTTTCCAGGACCCATCGAAG 998  
Db 884 GACATCTAGGTTCTGTAGTGAGCAGATCCAGAAATTTTCCAGGACCCATCGAAG 943  
QY 999 CGTGCAATCAATGCCACATCTTCTACGTACATCCGTAAGCTGGGACAAAGCCAGAG 1058  
Db 944 CGTGCAATCAATGCCACATCTTCTACGTACATCCGTAAGCTGGGACAGAGCCAGAG 1003  
QY 1059 GTGAGAGGCGCTTCCAGGAGGTATGACCCGTATAGCCACCCAGGCGCTTGGAGATGAC 1118  
Db 1004 GTGAGAGGCGCTTCCAGGAGGTATGACCCGTATAGCCACCCAGGCGCTTGGAGATGAC 1063  
QY 1119 CAGTCCCGCAAGTGTGAAACCAAGTAGATGCCAAGGAGGCGAAGTGGACTGCTCC 1178  
Db 1064 CAGTCTCCCAAGTGTGAAACCAAGTAGATGCCAAGGAGGCGAAGTGGACTGCTCC 1123  
QY 1179 GGTCTTCTTCTTCTCCAGGCGCTTTTGGTCTCTTCTCTGGATCCTTGTCTCCAGACTGGC 1238  
Db 1124 AGCTTTTCTTCTTCTCCAGGCGCTTTTGGTCTCTTCTCTGGATCCTTGTCTCCCGGACTGGC 1183  
QY 1239 CTCTGCTGAAAGTCTGAGAC--TGGGTGTGATGCAATGGCACTAGGGTACGGGCTTCC 1296  
Db 1184 CTCTGTTGAAAGTCTGAGACCGTGGGTGTGATGCAATGGCACTAGGGTATGGGCTTCC 1243  
QY 1297 CAGTATGTCCCCAGGCTCTATTCTTACCTATGGTGGAGCTCCCTTTCCCATGTGCTG 1356  
Db 1244 AAGTATGTCCCC-----AGCCTCTGTCTTTGTGCTG 1276  
QY 1357 CAACCTCTATGAAACTGAGGAGTGTCAAAGTGGACTTGGGAGCCATCTCTCTCTGC 1416  
Db 1277 CAACCTCTATGAAACTGAGGAGTGTCAAAGTGGACTTGGGAGCCATCTCTCTCTGC 1336  
QY 1417 ACCTTGCACGAAACACATGCAATGTGTGGCTGTCTGTCTTTCTGCTGCTGGGTGCTCC 1476  
Db 1337 ACCTTGCACGCAATATGCAATGTGTGGCTGTCTGTCTTTCTGCTGCTGGGTGCTCC 1396  
QY 1477 TGCTTGTGTGGCGCTTGTAGTCTCTCTTCTTCTTCTTAAACCAATAAAGACAAACAGACCA 1536  
Db 1397 TGCTTGTGTGTAGCGCTTGTAGTCTCTCTCTCTTCCACCAATAAAGACAAACAGACAA 1456

RESULT 2  
US-10-425-114-26649  
; Sequence 26649, Application US/10425114  
; Publication No. US2004003488A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT FILING DATE: 2003-04-28  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 26649  
; LENGTH: 1452  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Clone ID: L1B4653-002-F12\_FLI  
US-10-425-114-26649

|                       |      |  |                     |                 |                    |
|-----------------------|------|--|---------------------|-----------------|--------------------|
| Query Match           |      | 58.28;   | Score 903.8;        | DB 17;          | Length 1452;       |
| Best Local Similarity |      | 79.9%;   | Pred. No. 1.1e-269; |                 |                    |
| Matches 1131;         |      | Conservative   | 0;                  | Mismatches 267; | Indels 17; Gaps 5; |
| Qy                    | 94   | GGGTGCGAGACATGCTGCTGCTCAAGAAACAGACGAGGAGGACATCAGCAGTGTCTATGAGA | 153                 |                 |                    |
| Db                    | 6    | GGGACGGGACATGCTGCTGCTGAGAAACACACGGAGGACATCAGCAGGCTTACGAGA      | 65                  |                 |                    |
| Qy                    | 154  | TCCGGGAGAAAGCTGGGGTTCGGGCTCTTCTGAGGTGATGCTGGCCACGAAAGGGGCT     | 213                 |                 |                    |
| Db                    | 66   | TCCGCGAGAGGCTCGGGTCGGGCTCTTCCGAGGTGGTGTCTGGCCACGAGCGGGCT       | 125                 |                 |                    |
| Qy                    | 214  | CTGCTCATCTTGTGGCCCTCAAGTGCATTCACCAAGAAAGCACTTCGGGGCAAGAGGCC    | 273                 |                 |                    |
| Db                    | 126  | CCGACACCTCGTGGCCCTCAAGTGCATTCACCAAGAAAGGCCCTCCGGGGCAAGAGGCC    | 185                 |                 |                    |
| Qy                    | 274  | TGGTGGAGAATGAGATCGCGTACTTCGCAAGATCAGCCATCCCAACATTTGTGCTCTGG    | 333                 |                 |                    |
| Db                    | 186  | TGGTGGAGAAGAGATCGAGTGTCTCGTAGGATCAGTCAACCCACATCGTCTCTGG        | 245                 |                 |                    |
| Qy                    | 334  | AGGACGTCATGAGAGTCTTCTCATCTCTACTTGGCCATGGAGCTGTTAACAGGTGGT      | 393                 |                 |                    |
| Db                    | 246  | AGGATGTCCACGAGAGCCCTTCCACCTCTACCTGGCCATGGAACCTGTTGAGGGTGGG     | 305                 |                 |                    |
| Qy                    | 394  | AACGTTTACCGCATCATGAGCGGGCTCTACACAGAGAGGACGCCAGCACCTTG          | 453                 |                 |                    |
| Db                    | 306  | AGCTGTTTACCGCATCATGAGCGGGCTCTACACAGAGAGGATGCCAGCCATCTGG        | 365                 |                 |                    |
| Qy                    | 454  | TAGGGAGGTCTTTGGGCTGTCTCTACCTTATAGCTGGGCATCGTGCACCGGGACC        | 513                 |                 |                    |
| Db                    | 366  | TGGTCAAGTCTTTGGGCGCGTCTCTACCTGACAGCCCTGGGATCGTGACCGGGACC       | 425                 |                 |                    |
| Qy                    | 514  | TCAAGCTCGAAACCTCTCTATGCCACACCTTTTGGAGTCTCAAGATCATGTCTCTG       | 573                 |                 |                    |
| Db                    | 426  | TCAAGCCGGAACCTCTCTATGCCACGCGCTTTGAGGACTCGAAGATCATGTCTCTG       | 485                 |                 |                    |
| Qy                    | 574  | ACTTTGGCTGTCCAAATCAAGCTGGCAACATCTAGGACAGCCTGTGGACCCCG          | 633                 |                 |                    |
| Db                    | 486  | ACTTTGACTCTCCAAATCAGGCTGGGAACATCTAGGACCGCTGTGGACCCCGT          | 545                 |                 |                    |
| Qy                    | 634  | GATATGGCCCCAGAGCTCTGGAGCAGAAACCTTACGGGAGGCCGTAGATGTGGG         | 693                 |                 |                    |
| Db                    | 546  | GATATGGCCCCAGAGCTCTGGAGCAGAAACCTTACGGGAGGCCGTAGATGTGGG         | 605                 |                 |                    |
| Qy                    | 694  | CCCTGGGTGTCTCTCTACATCTGCTGTGTGGGTACCCCGCTTCTATGATGAGAGCG       | 753                 |                 |                    |
| Db                    | 606  | CCCTGGGCTCACTCTCTACATCTGCTGTGTGGGTACCCCGCTTCTACAGAGAGCG        | 665                 |                 |                    |
| Qy                    | 754  | ATCCTGAATCTTTCAGCCAGATCTGAGGGCCAGCTATGATTTGACTCCCGCTTTTGGG     | 813                 |                 |                    |
| Db                    | 666  | ACCTGAGCTCTTCAGCCAGATCTGAGGGCCAGCTATGATTTGACTCTCTTCTGGG        | 725                 |                 |                    |
| Qy                    | 814  | ATGACATCTCAGATCAGCCAAAGACTTCATTGCGACCTTCTGGAAAGTATCCCCAGA      | 873                 |                 |                    |
| Db                    | 726  | ATGACATCTCAGATCAGCCAAAGACTTCATTGCGACCTTCTGGAGGAGACCCCCAGA      | 785                 |                 |                    |
| Qy                    | 874  | AGAGGTTCACTGCGACAGCCCTACAGCATCTTTGATCTCTGCGGATGACGCTTTCG       | 933                 |                 |                    |
| Db                    | 786  | AGAGGTTCACTGCGCAACAGCCCTTGGACCTTTGGATCTCTGGGACACAGCCCTTCG      | 845                 |                 |                    |
| Qy                    | 934  | ATAGGACATCTCGGGTCTGTCTCAGTGAGCAGATCCAGAAAGATTTTTCAGGACCCACT    | 993                 |                 |                    |
| Db                    | 846  | ACAGGACATCTTAGGCTGTCTCAGTGAGCAGATCCGGAAGACTTTTGTCTCGGACACT     | 905                 |                 |                    |
| Qy                    | 994  | GGAAGCGTGATTCATGCGACATCATCTCTTAAGTCAATCCGTAAGCTGGGACAAAGCC     | 1053                |                 |                    |
| Db                    | 906  | GGAAGCGAGGCTTCAATGCCACCTCTGTTCTCTGCGCCACATCCGGAAGCTGGGGCAGATCC | 965                 |                 |                    |
| Qy                    | 1054 | CAGAGGTGAGGAGGCTCCAGGAGTGTATGACCGCTATAGCCACCCAGG-CTTTGGG       | 1112                |                 |                    |
| Db                    | 966  | CAGAGGCGAGGGGCTCTGAGCAGGGCATGGCCCGCCACAGCACTCAGGCGCCCTCGT      | 1025                |                 |                    |
| Qy                    | 1113 | ACTAGCCAGTCCCCCAAGTGGTGAACACCCAGGTAGATGCCAAGGAAGGCCAAGTGGACTG  | 1172                |                 |                    |

|  |      |  |      |  |  |
|--|------|--|------|--|--|
| Db   | 1026 | GCTGGCCAGCCCCCAAGTGGTATGCCAGGAGATGCC-----GAGGCCAAGTGGACTG      | 1081 |  |  |
| Qy   | 1173 | ACTCCCGGTTTTTCTTTCTCTCCAGCCCTTTTGGTCTCTTTCTCTGGATCCTTGTCTCCAG  | 1232 |  |  |
| Db   | 1082 | ACCCCCAGATTTCTTCTCCCTGGATGCTTTCCGTCCTCCCAACCCCTCCCGCTGGG       | 1141 |  |  |
| Qy   | 1233 | ACTGGCCTCTGCTGGAAAGTCTGA-GACTGGGTGTGATGATGGCACTAGGGT-----ACG   | 1287 |  |  |
| Db   | 1142 | GCTGGCCTCTGCTGGATTTTGGATTTTGGGGTGTGGCGATGGCGCTGGGGTTGGAATG     | 1201 |  |  |
| Qy   | 1288 | GGGCTTCCCGAGTATGTCGCCCGCAGCTCTATTCTTACCTATGTGTGGAGGCTCCCTTTCCC | 1347 |  |  |
| Db   | 1202 | GGGACCCCCAAGTGTGTCCCGAGGCTCTGCCCTGCCCTGGGGGAGTGGCTCCCGCTCCC    | 1261 |  |  |
| Qy   | 1348 | ATGTGCTGCGCCACCTCTATGAAACTGAGGAGGTGTTCAAAAGTGAACCTTGGAGGCCAT   | 1407 |  |  |
| Db   | 1262 | TGTTGCTCTCTCGCCCTGTCGCCCGCCCGCCCGCCCAAGACCGAGGGGTGCTGGCAGG     | 1321 |  |  |
| Qy   | 1408 | CTTCTGCACTTGTGCAAGAACATGATGTGTGTGGCTGTCTGTGCTTTGCTGACTGT       | 1467 |  |  |
| Db   | 1322 | CGGGCC-----TCAGGGGCTGTCTTTCTCTGCACGGCTGTGTGTGCTTGGCTGAGTGT     | 1374 |  |  |
| Qy   | 1468 | GGGTGCTCTGCTGTGTGTGTGGCCCTTTAGTTCC                             | 1502 |  |  |
| Db   | 1375 | GGGTGCTCTGCTGT     | 1409 |  |  |
| RESULT 3   |      |  |      |  |  |
| US-10-302-172-205  |      |  |      |  |  |
| ; Sequence 205, Application US/10302172  |      |  |      |  |  |
| ; Publication No. US20040053250A1  |      |  |      |  |  |
| ; GENERAL INFORMATION:   |      |  |      |  |  |
| ; APPLICANT: Tang, Y. Tom  |      |  |      |  |  |
| ; APPLICANT: Dmanac, Radoje T.   |      |  |      |  |  |
| ; TITLE OF INVENTION: No. US20040053250A1el Arginine-rich Protein-like Nucleic Acids |      |  |      |  |  |
| ; TITLE OF INVENTION: Polypeptides   |      |  |      |  |  |
| ; FILE REFERENCE: 803 1CNGP  |      |  |      |  |  |
| ; CURRENT APPLICATION NUMBER: US/10/302,172  |      |  |      |  |  |
| ; PRIOR FILING DATE: 2002-11-21  |      |  |      |  |  |
| ; PRIOR APPLICATION NUMBER: US 10/225,251  |      |  |      |  |  |
| ; PRIOR FILING DATE: 2002-08-20  |      |  |      |  |  |
| ; PRIOR APPLICATION NUMBER: PCT US02/05095   |      |  |      |  |  |
| ; PRIOR FILING DATE: 2002-03-05  |      |  |      |  |  |
| ; PRIOR APPLICATION NUMBER: US 09/799,451  |      |  |      |  |  |
| ; PRIOR FILING DATE: 2001-03-05  |      |  |      |  |  |
| ; NUMBER OF SEQ ID NOS: 950  |      |  |      |  |  |
| ; SOFTWARE: pt_FL_genes Version 2.0  |      |  |      |  |  |
| ; SEQ ID NO 205  |      |  |      |  |  |
| ; LENGTH: 1584   |      |  |      |  |  |
| ; TYPE: DNA  |      |  |      |  |  |
| ; ORGANISM: Homo sapiens   |      |  |      |  |  |
| ; FEATURE:   |      |  |      |  |  |
| ; NAME/KEY: CDS  |      |  |      |  |  |
| ; LOCATION: (51)..(1166)   |      |  |      |  |  |
| US-10-302-172-205  |      |  |      |  |  |
| Query Match  |      |  |      |  |  |
| Best Local Similarity 55.3%; Score 859; DB 17; Length 1584;                          |      |  |      |  |  |
| Matches 1098; Conservative 0; Mismatches 270; Indels 27; Gaps 5;                     |      |  |      |  |  |
| Qy   | 168  | GGCTCGGGTGCCTTCTCTGAGGTGATGCTGGCCAGGAAAGGGCTCTGTCTATCTTGTG     | 227  |  |  |
| Db   | 201  | GGCAGGGGTGCCTTCTCCGAGGTGTGCTGGCCAGAGCGGGCTCCGCACACCTCGT        | 260  |  |  |
| Qy   | 228  | GCCTCAAGTGCATTTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTTGTGGGAATGAG    | 287  |  |  |
| Db   | 261  | GCCTCAAGTGCATTTCCCAAGAAAGGCCCTTCGGGGCAAGGAGGCCCTTGTGGGAATGAG   | 320  |  |  |
| Qy   | 288  | ATCGGGTACTTCGCAAGATCAGCCATCCCAATTTGTGGCTCTGGAGGACGTCATGAG      | 347  |  |  |
| Db   | 321  | ATCGAGTGTCTCGTAGGATCAGTCAACCAACATCGTCTGTGGAGGATGTCCAGAG        | 380  |  |  |

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QY 348 AGTCTCTTCATCTTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTGTTTGACCGC 407
Db 381 AGCCCTTCCACCTTCTTACCTGGCCATGGAACTGGTGACGGGTGGCAGCTGTTTGAACCGC 440
QY 408 ATCATGAGGGGGCTTCTACACAGAGAAGAGCGCCAGACCCTCTGTAGGGCAGGTCCCTT 467
Db 441 ATCATGAGGGCGGGCTTCTACACAGAGAAGAGTCCAGGCCATCTGGTGGGTGAGTCCCTT 500
QY 468 GCGCTGTCTCTTACCTTCTATAGCCTGGGCATCGTGCCAGCGGACCTCAAGCCTGAAAC 527
Db 501 GCGCCGCTCTCTTACCTGCACAGCCTGGGGATCGTGCCAGCGGACCTCAAGCCCGGAAAC 560
QY 528 CTCCTATGCCACACCTTTTGGAGCTCAAAGATCATGTGTCTCTGACTTTGGCCCTGTCC 587
Db 561 CTCCTGTATGCCAGCCCTTTGGAGCTCGAAGATCATGTGTCTCTGACTTTGGACTCTCC 620
QY 588 AAAATACAAGCTGCAACATGCTAGGCACAGCCTGTGGGACCCAGGATATGGGCCCA 647
Db 621 AAAATCAGGCTGGGAACATGCTAGGCACCGCTGTGGGACCCCTGGATATGTGGCCCA 680
QY 648 GAGCTCTGTGAGCAGAAACCTTACGGGAAGCGGTAGATGTGTGGCCCTGGGTGTCTATC 707
Db 681 GAGCTCTTGGAGCAGAAACCTTACGGGAAGCGGTAGATGTGTGGCCCTGGGCGTCTATC 740
QY 708 TCCTACATCTGTGTGTGGGTACCCCTTCTATGATGAGAGCGATCTGAACCTCTTC 767
Db 741 TCCTACATCTGTGTGTGGGTACCCCTTCTATGATGAGAGCGATCTGAACCTCTTC 800
QY 768 AGCCAGATCTGAGGCGCAGCTATGAGTTGATCTCCCTTTTGGGATGACATCTCAGAA 827
Db 801 AGCCAGATCTGAGGCGCAGCTATGAGTTGATCTCTCTTCTGGGATGACATCTCAGAA 860
QY 828 TCAGCCAAAGACTTCAATTCGCCACCTTCTTGGAACTGATCCCGAAGAGGTTTCACTGC 887
Db 861 TCAGCCAAAGACTTCAATTCGCCACCTTCTTGGAGCGAGACCCCGAAGAGGTTTCACTGC 920
QY 888 CAGCAGGCCCTACAGCATCTTTGATCTCTGGGGATGACGCTTCGATAGGGACATCTCTG 947
Db 921 CAACAGGCCCTTGGGCACTTGGATCTCTGGGGACACAGCCTTCGACAGGACATCTTA 980
QY 948 GGTCTGTGTCAGTGAGCAGATCCAGAGAAATTTTGGCAGGACCCACTGGAAGCGTGATTC 1007
Db 981 GGCTGTGTAGTGAGCAGATCCGGAAGAACTTTGTCTGGACACACTGGAAGCGAGCCTTC 1040
QY 1008 AATGCCACATCTTCTTACGTTCATCCGTAAAGCTGGGAACAAAGCCAGAGGCTGAGGAG 1067
Db 1041 AATGCCACCTCTGTTCTCGCCACATCCGGAAGCTGGGCGAGATCCAGAGGGCGAGGG 1100
QY 1068 GCCTCCAGGAGTGATGACCCGTCATAGCACCCAGGCTTGGGACTAGCCAGTCCCCC 1127
Db 1101 GCCTCTGAGCAGGCGATGGCCCGCCACAGCACTCAGGCTCTCGGTGTCGCCAGCCCCC 1160
QY 1128 AGTGGTGAACACAGGTAGATGCCAGGAAGGCCAAGTGAAGTGAAGTCCCGGTTTCT 1187
Db 1161 AAGTGGTGAAGTCCAGGACAGATGCC-----GAGGCGAAGTGAAGTGAAGTCCCGGTTTCT 1216
QY 1188 TTCTCTCAGCCCTTTTGGTCTTCTTCTGTGATCTTGTCTCCAGACTGGCCCTCTGTGG 1247
Db 1217 TCCTTGGATGCTTTCGTCTCCCTCCCAACCCCTCCCTGGGGCTGGCCCTCTGTGG 1276
QY 1248 AAAGTCTGA-GACTGGGTGTGATGATGGCACTAGGCT----ACGGGGCTTCCCCAGTAT 1302
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QY 1303 GTCCCCAGCCTTATTTCTTACCTATGATGGAGGCTCCCTTCCCATGTCTGCGCCACC 1362
Db 1337 TGTCCTCAGGCTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1396
QY 1363 TCTATGAAACTGAGGAGGTGTTCAAAAGTGAAGTCTGGGAGGCCATCTTCTCTGCACTTG 1422
Db 1397 CCCTGCCCCCCCCCGCCCAAAAGCGGAGGGGTCTGCGAGGGGGC-----TC 1449
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1423 CACGAACACATGATTGTGTGGCTGTCTGTGCTTTGCTGACTGTGGTGGTCTGCTTGG 1482

1450 AGGGCTGTCTTCTTGTGACGGCTGTGTGTGCTTGTGCTGAGTGTGGTGGTCTGCTTGG 1509

1483 TGTGTGGCCCTTTAGTTCCTCC-----TTTCTTACCAATAAAGACAACAG 1531

1510 TGTGATGTCATGGCTTCCAGGCCCTCCAGCTTTTCCCAACCAATAAAGAAAGATAC 1569

1532 AACCAAAAAAAAAA 1546

1570 AGCAAAAAAAAAA 1584

RESULT 4

US-09-769-970-12

Sequence 12, Application US/09769970

Publication No. US20030170219A1

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

Hillman, Jennifer L.

Corley, Neil C.

Guegler, Karl G.

Lal, Preeti

Goli, Surya K.

Shah, Purvi

TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN KINASES

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/769,970

FILING DATE: 24-Jan-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/272,796

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J J

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0321 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 1282 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: PROSNOT06

CLONE: 827431

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-769-970-12

Query Match 54.3%; Score 844.4; DB 10; Length 1282;

Best Local Similarity 86.2%; Pred. No. 3.1e-251;

Matches 940; Conservative 1; Mismatches 145; Indels 4; Gaps 1;

QY 101 AGACATGCTGCTCTCAAGAAACAGCGGAGGACATCAGCAGTGTCTTATGAGATCCGGGA 160

Db 197 AAACATGCTGCTGCTGAGAAAACACACGAGGAGCATCAGCAGCGTCTACAGATCCCGA 256  
Qy 161 GAAGCTGGGCTCGGGTCTCTCTGTAGGTGATGCTGGCCCGAGAAAGGGGCTCTGTCTCA 220  
Db 257 GAGGCTCGGCTCGGGTCTCTCCGAGGTGGTCTGGCCCGAGGCGGGCTCCGCACA 316  
Qy 221 TCTTGTGGCCCTCAAGTGCAATCCCAAGAAAGCACTTCGGGGCAAGAGGCCCTGTGGGA 280  
Db 317 CCTGTGGCCCTCAAGTGCAATCCCAAGAAAGGCCCTCGGGCAAGAGGCCCTGTGGGA 376  
Qy 281 GAATGAGATCGCGTACTTCGCAAGATCAGCAATCCCAATGTTGGCTCTGTAGGAGCGT 340  
Db 377 GAACGAGATCGCAGTGTCTCGTAGGATCAGTACCCCAACATCGTCTGTGAGGATGT 436  
Qy 341 CCATGAGATCCTTCTCATCTCTACTTGGCCATGAGCTGGTAACAGGTGGTGAATGTT 400  
Db 437 CCACGAGAGCCCTTCCACCTTACCTTGGCCATGGAATGTTGACGGTGGCGAGCTGTT 496  
Qy 401 TGACCGCATCATGAGCGGGGCTCTTACAGAGAAGGACGCCAGCCACTTGTAGGGCA 460  
Db 497 TGACCGCATCATGAGCGGGGCTCTTACAGAGAAGGATGCCAGCCACTTGTGGGTCA 556  
Qy 461 GGTCTTGGCGCTGCTCTCTACCTTCTATGAGGATCCCAAGATCATGTCTCTGACTTTGG 520  
Db 557 GGTCTTGGCGCGTCTCTCTACCTTCTATGAGGATCCCAAGATCATGTCTCTGACTTTGG 616  
Qy 521 TGAAGACCTCTCTATGCCACACCTTTGAGGATCCCAAGATCATGTCTCTGACTTTGG 580  
Db 617 CGAAACCTCTCTATGCCACGCGCTTTGAGGATCCCAAGATCATGTCTCTGACTTTGG 676  
Qy 581 CCTGTCAAATAACAGCTGGCAACATGCTAGGACAGCCTGTGGGACCCAGATATGT 640  
Db 677 ACTCTCAAATAACAGCTGGCAACATGCTAGGACAGCCTGTGGGACCCCTGTGATATGT 736  
Qy 641 GGCCCAAGCTCTCTGAGCAGAAACCTTACGGGAGGCGGTAGATGTGGGCGCTGGG 700  
Db 737 GGCCCAAGCTCTTGGAGCAGAAACCTTACGGGAGGCGGTAGATGTGGGCGCTGGG 796  
Qy 701 TGTCTATCTCTACATCTCTGTGTGGGTACCCCGCTTCTATGATGAGAGCGATCTCTGA 760  
Db 797 CGTCACTCTCTACATCTCTGTGTGGGTACCCCGCTTCTACGAGAGAGCGACCTCTGA 856  
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Qy 821 CTGAGATCAGCAAGACTTCTTCCACCTTCTGGAACGTGATCCCGCAGAGAGTT 880  
Db 917 CTGAGATCAGCAAGACTTCTTCCACCTTCTGGAACGTGATCCCGCAGAGAGTT 976  
Qy 881 CACTGCGACGAGCCCTACAGCATCTTTGGATCTCTGGGATGCGAGCTTTCGATAGGGA 940  
Db 977 CACTGCGACAGCCCTTGGGACCTTTGGATCTTTTGGACACAGGCTTTGGCAGGGA 1036  
Qy 941 CATCTCTGGGTCTGTAGTGAGCAGATCCAGAGAAATTTTCCAGGACCCACTGGAGCG 1000  
Db 1037 CATCTTGGGTCTGTAGTGAGCAGATCCAGAGAACTTTTCTTGGACACACTGGAGCG 1096  
Qy 1001 TGCAATCAATGCCACATCATCTCTAAGTCAATCCGTAAGCTGGGACAAAGCCAGAGG 1060  
Db 1097 AGCCTTCAATGCCACCTTGTCTCTGCGCCACATCCGGAAGCTGGGGCAGATCCAGAGG 1156  
Qy 1061 TGAGGAGCCCTCAGGCGAGTGTATGACCTCTATAGCCACCCAGGCTTGGGATAGCCA 1120  
Db 1157 CGAGGGGCTCTGTAGCAGGCAATGAGCCGNCACAGCCACTNAGGCTTCTGTGTGGCCA 1216  
Qy 1121 GTCCCCAAGTGTGAAACAGAGTATGCTCAAGGAGGCGCAAGTGGACTGACTCCCGG 1180  
Db 1217 GCCCCCAAGTGTGATGCCAGGAGATGCC----GAGGCCAAGTGGANTGACCCAG 1272  
Qy 1181 TTTTCTTCTTC 1190  
Db 1273 ATTCTTCTTC 1282

RESULT 5

US-10-305-720-953  
; Sequence 953, Application US/10305720  
; Publication No. US20040010136A1  
; GENERAL INFORMATION:  
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.  
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression  
; FILE REFERENCE: PA-0002-1 CON  
; CURRENT APPLICATION NUMBER: US/10/305,720  
; CURRENT FILING DATE: 2002-11-26  
; PRIOR APPLICATION NUMBER: 09/016,434  
; PRIOR FILING DATE: 1998-01-30  
; NUMBER OF SEQ ID NOS: 1490  
; SOFTWARE: PERL Program  
; SEQ ID NO 953  
; LENGTH: 1282  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20040010136A1 827431  
; NAME/KEY: unsure  
; LOCATION: (1) ... (1282)  
; OTHER INFORMATION: a, t, c, g, or other  
US-10-305-720-953

Query Match 54.3%; Score 844.4; DB 17; Length 1282;  
Best Local Similarity 86.2%; Pred. No. 3.1e-251;  
Matches 940; Conservative 1; Mismatches 145; Indels 4; Gaps 1;

Qy 101 AGACATGCTCTCTCTCAAGAAACAGACGAGGAGCATCAGCAGTGTCTATGATCCGGA 160  
Db 197 AAACATGCTCTCTCTGAAGAAACACACGAGGAGCATCAGCAGGCTCTACGAGATCCGGA 256  
Qy 161 GAAGCTGGGCTCGGGTCTCTCTGTAGGTGATGCTGGCCCGAGAAAGGGGCTCTGTCTCA 220  
Db 257 GAGGCTCGGCTCGGGTCTCTCTCGAGGTGGTGTGGTGGCCCGAGGCGGGCTCCGCACA 316  
Qy 221 TCTTGTGGCCCTCAAGTGCAATCCCAAGAAAGCACTTCGGGGCAAGAGGCCCTGTGGGA 280  
Db 317 CCTGTGGCCCTCAAGTGCAATCCCAAGAAAGGCCCTCCGGGGCAAGAGGCCCTGTGGGA 376  
Qy 281 GAATGAGATCGCGTACTTCGCAAGATCAGCAATCCCAATGTTGGCTCTGTAGGAGCGT 340  
Db 377 GAACGAGATCGCAGTGTCTCGTAGGATCAGTACCCCAACATCGTCTCTGTGAGGATGT 436  
Qy 341 CCATGAGATCCTTCTCATCTCTACTTGGCCATGAGCTGGTAACAGGTGGTGAATGTT 400  
Db 437 CCACGAGAGCCCTTCCACCTTCTACCTGGCCATGGAATGTTGACGGTGGCGAGCTGTT 496  
Qy 401 TGACCGCATCATGAGCGGGGCTCTTACAGAGAAGGACGCCAGCCACTTGTAGGGCA 460  
Db 497 TGACCGCATCATGAGCGGGGCTCTTACAGAGAAGGATGCCAGCCACTTGTGGGTCA 556  
Qy 461 GGTCTTGGCGCTGCTCTCTACCTTCTATAGCTGGGATCGTGCACCGGACCTCAAGCC 520  
Db 557 GGTCTTGGCGCGTCTCTCTACCTTCTATGCAAGCTGGGGATCGTGCACCGGACCTCAAGCC 616  
Qy 521 TGAAGACCTCTCTATGCCACACCTTTTGGAGGACTCCCAAGATCATGTCTCTGACTTTGG 580  
Db 617 CGAAACCTCTCTATGCCACGCGCTTTGAGGATCCCAAGATCATGTCTCTGACTTTGG 676  
Qy 581 CCTGTCAAATAACAGCTGGCAACATGCTAGGACAGCCTGTGGGACCCAGGATATGT 640  
Db 677 ACTCTCAAATAACAGCTGGGAAACATGCTAGGACAGCCCTGTGGGACCCCTGTGATATGT 736  
Qy 641 GGCCCAAGCTCTCTGAGCAGAAACCTTACGGGAGGCGGTAGATGTGGGCGCTGGG 700  
Db 737 GGCCCAAGCTCTTGGAGCAGAAACCTTACGGGAGGCGGTAGATGTGGGCGCTGGG 796

QY 701 TGTCTCTCTATCATCTCTGCTGTGGTGTACCCCTCTCTATGATGAGAGCATCTCTGA 760  
DB 797 CGTCATCTCTATCATCTCTGCTGTGGTGTACCCCTCTCTACGACGAGAGCATCTCTGA 856  
QY 761 ACTCTTCAGCCAGATTCCTGAGGCGCAGCTATGAGTTTGACTCCCTCTTTTGGGATGACAT 820  
DB 857 GCTCTTCAGCCAGATTCCTGAGGCGCAGCTATGAGTTTGACTCTCTTTCTGGATGACAT 916  
QY 821 CTCAGAAATCAGCAAGACTTCATTCGCCACCTTCCTGGAACTGGAACTGGAACTGGAACTGGAA 880  
DB 917 CTGAGAAATCAGCAAGACTTCATTCGCCACCTTCCTGGAACTGGAACTGGAACTGGAACTGGAA 976  
QY 881 CACCTGCCAGCAGGCGCTACAGCATCTTTGGATCTCTGGGATGAGCCTTCGATAGGGA 940  
DB 977 CACCTGCCAAGCAGGCGCTTCGGGACCTTTGGATCTTTTGGGACACAGGCTTTGGGAGGGA 1036  
QY 941 CATCTCTGGGTTCTGTCAGTGAGCAGATCCAGAAAGAAATTTTGGCAGCACCACCTGGAAAGCG 1000  
DB 1037 CATCTTAGGTTTCTGTCAGTGAGCAGATCCGGAAGAACTTTGCTTGGACACACTGGAAAGCG 1096  
QY 1001 TGCAATTCATTCGCACATCATCTCTACGTCAATCCGTAAGCTGGGAACAAAGCCAGAGGG 1060  
DB 1097 AGCTTTCAATGCGACCTTTGCTCTGCGCCACATCCCGAAGCTGGGCGAGATCCAGAGGG 1156  
QY 1061 TGAGGAGGCGCTCAGGAGGTGTATGACCGTCTATAGCCACCAGGCGCTTGGGACTAGCCA 1120  
DB 1157 CGAGGGGCGCTCTGAGCAGGCGCATGSGCCGNCACAGCCACTNAGGCGCTTCTGCTCTGGCCA 1216  
QY 1121 GTCCCCCAAGTGTGAAGAACAGGTAGATGCCAAGGAAGCCCAAGTGGAGTGAAGTCCCGG 1180  
DB 1217 GCCCCCCAAGTGTGATGCCAGNAGATGCC-----GAGGCCAAGTGGANTGANCCCCAG 1272  
QY 1181 TTTTCTTCTTC 1190  
DB 1273 ATTTCNTTNC 1282

## RESULT 6

US-10-656-598-5  
; Sequence 5, Application US/10656598  
; Publication No. US20040229232A1  
; GENERAL INFORMATION:  
; APPLICANT: DAVID P. DAVIS  
; APPLICANT: FREDERIC J. DESAUVAGE  
; APPLICANT: WILLIAM I. WOOD  
; APPLICANT: ZEMIN ZHANG  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
; TITLE OF INVENTION: TREATMENT OF TUMOR  
; FILE REFERENCE: P1981R1P1-US  
; CURRENT APPLICATION NUMBER: US/10/656,598  
; CURRENT FILING DATE: 2003-09-05  
; PRIOR APPLICATION NUMBER: US 60/410,166  
; PRIOR FILING DATE: 2002-09-11  
; NUMBER OF SEQ ID NOS: 52  
; SEQ ID NO 5  
; LENGTH: 1282  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: Unsure  
; LOCATION: 898, 1187, 1198, 1241, 1262, 1266, 1277, 1281  
; OTHER INFORMATION: Unknown base  
US-10-656-598-5

Query Match 54.3%; Score 844.4; DB 18; Length 1282;  
Best Local Similarity 86.2%; Pred. No. 3.1e-251;  
Matches 940; Conservative 1; Mismatches 145; Indels 4; Gaps 1;  
QY 101 AGACATCTGCTGCTCAAGAAACACAGCGGAGGACATCAGCAGTGTCTATGAGATCCGGGA 160  
DB 197 AAACATCTGCTGCTGAAGAAACACACGAGGAGCATCAGCAGCGTCTACGAGATCCGCGA 256  
QY 161 GAAGCTGGGCTCGGGTCTCTCTGAGGTGATGCTCGGCCCAAGAAAGGGGCTCTGTCTCA 220

DB 257 GAGGCTCGGCTCGGGTGCCTTCTCGAGGTGTGTGCTGCGCCAGGAGCGGGCTCCGCACA 316  
QY 221 TCTTGTGGCCCTCAAGTGCATTTCCAAAGAAAGCACTTCGGGGCAAGAGGCCCTGTGTGGA 280  
DB 317 CCTGTGGCCCTCAAGTGCATTTCCAAAGAAAGGCCCTTCGGGGCAAGAGGCCCTGTGTGGA 376  
QY 281 GAATGAGATCGGGTACTTTCGAGATCAGCCATCCCAACATTTGCTGCTCTGAGACCT 340  
DB 377 GAACGAGATCGCAGTCTCCGTAGGATCAGTCAACCAACATCGTCTCTGAGGATGT 436  
QY 341 CATGAGAGTCTCTCTCATCTCTACTTGGCCATGGAGCTGGTAAACAGGTGGTAACTGTT 400  
DB 437 CCAAGAGGCCCTTCCCACTCTACTTGGCCATGGAGCTGGTAAACAGGTGGTAACTGTT 496  
QY 401 TGACCGCATCATGGAGCGGGCTCTCTACAGAGAAAGGACGCGAGCCACTTGTAGGGCA 460  
DB 497 TGACCGCATCATGGAGCGGGCTCTCTACAGAGAAAGGATGCCAGCATCTGTGGGTCA 556  
QY 461 GGTCTTGGCGCTCTCTCTACCTTATAGCTTGGGCATCGTGCAAGGAGCCCTCAAGCC 520  
DB 557 GGTCTTGGCGCGCTCTCTCTACCTTATAGCTTGGGCATCGTGCAAGGAGCCCTCAAGCC 616  
QY 521 TGAAGAACCTCTCTATGCCACACCTTTTGGAGACTCCAAGATCATGCTCTCTGACCTTTGG 580  
DB 617 CGAAGAACCTCTCTGATGCCACCGCTTTGAGGACTCGAAGATCATGCTCTGACCTTTGG 676  
QY 581 CCTGTCAAAATACAGCTGGCAACATCTTAGGACACAGCTGTGGACCCCAAGATATGT 640  
DB 677 ACTCTCAAAATCCAGGCTGGGAAACATGCTAGGACCGCTGTGGACCCCTCGATATGT 736  
QY 641 GGGCCAGAGCTCTGGAGCAGAAACCTTACGGGAAGGCGGTAGATGTGTGGGCCCTGGG 700  
DB 737 GGGCCAGAGCTCTGGAGCAGAAACCTTACGGGAAGGCGGTAGATGTGTGGGCCCTGGG 796  
QY 701 TGTCTCTCTATCATCTCTGCTGTGGTGTACCCCTCTCTATGATGAGAGCATCTCTGA 760  
DB 797 CGTCATCTCTATCATCTCTGCTGTGGTGTACCCCTCTCTACGACGAGAGCATCTCTGA 856  
QY 761 ACTCTTCAGCCAGATTCCTGAGGCGCAGCTATGAGTTTGACTCCCTCTTTTGGGATGACAT 820  
DB 857 GCTCTTCAGCCAGATTCCTGAGGCGCAGCTATGAGTTTGACTCTCTTTCTGGGATGACAT 916  
QY 821 CTCAGAAATCAGCAAGACTTCATTCGCCACCTTCTGGAACGTGATCCCCCAGAGAGGTT 880  
DB 917 CTCAGAAATCAGCAAGACTTCATTCGCCACCTTCTGGAACGTGATCCCCCAGAGAGGTT 976  
QY 881 CACCTGCCAGCAGGCGCTTACAGCATCTTTGGATCTCTGGGGATGCGAGCTTTTCGATAGGGA 940  
DB 977 CACCTGCCAAGGCGCTTGGGACCTTTGGATCTTTTGGGACACAGGCTTTGGCAGGGA 1036  
QY 941 CATCTCTGGGTTCTGTCAGTGAGCAGATCCAGAAAGAAATTTTTCAGGACCCCACTGGAAAGCG 1000  
DB 1037 CATCTTAGGTTTGTTCAGTGAGCAGATCCGGAAGAACTTTGCTTGGACACACTGGAAGCG 1096  
QY 1001 TGCAATTCATGCGACATCATCTCTAGTCATCTCGTAAAGCTGGGACAAAGCCAGAGGG 1060  
DB 1097 AGCTTTCAATGCGCACCTTGTCTCTGCGCCACATCCCGGAAGCTGGGCGAGATCCCAGAGGG 1156  
QY 1061 TGAGGAGGCGCTCCAGGCGAGTGTATGACCCCTCATAGCCACCAGGCGCTTGGGACTAGCCA 1120  
DB 1157 CGAGGGGCGCTCTGAGCAGGCGCATGSGCCGNCACAGCCACTNAGGCGCTTCTGCTCTGGCCA 1216  
QY 1121 GTCCCCCAAGTGTGAAGAACAGGTAGATGCCAAGGAAGCCCAAGTGGAGTGAAGTCCCGG 1180  
DB 1217 GCCCCCCAAGTGTGATGCCAGNAGATGCC-----GAGGCCAAGTGGANTGANCCCCAG 1272  
QY 1181 TTTTCTTCTTC 1190  
DB 1273 ATTTCNTTNC 1282

## RESULT 7

US-10-643-795A-9  
; Sequence 9, Application US/10643795A  
; Publication No. US20040241703A1  
; GENERAL INFORMATION:  
; APPLICANT: FREDERIC J. DESAUVAGE  
; APPLICANT: GRETCHEN FRANTZ  
; APPLICANT: KENNETH J. HILLAN  
; APPLICANT: PAUL POLAKIS  
; APPLICANT: ANDREW POLSON  
; APPLICANT: VICTORIA SMITH  
; APPLICANT: SUSAN D. SPENCER  
; APPLICANT: THOMAS D. WU  
; APPLICANT: ZEMIN ZHANG  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
; TITLE OF INVENTION: TREATMENT OF TUMOR  
; FILE REFERENCE: P5026R1-US  
; CURRENT APPLICATION NUMBER: US/10/643,795A  
; CURRENT FILING DATE: 2003-08-19  
; PRIOR APPLICATION NUMBER: US 60/404,809  
; PRIOR FILING DATE: 2002-08-19  
; PRIOR APPLICATION NUMBER: US 60/405,645  
; PRIOR FILING DATE: 2002-08-21  
; PRIOR APPLICATION NUMBER: US 60/413,192  
; PRIOR FILING DATE: 2002-09-23  
; PRIOR APPLICATION NUMBER: US 60/419,008  
; PRIOR FILING DATE: 2002-10-15  
; PRIOR APPLICATION NUMBER: US 60/426,847  
; PRIOR FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/484,959  
; PRIOR FILING DATE: 2003-07-02  
; NUMBER OF SEQ ID NOS: 158  
; SEQ ID NO 9  
; LENGTH: 1282  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: Unsure  
; LOCATION: 898, 1187, 1198, 1241, 1262, 1266, 1277, 1281  
; OTHER INFORMATION: Unknown base  
US-10-643-795A-9

Query Match 54.3%; Score 844.4; DB 18; Length 1282;  
Best Local Similarity 86.2%; Pred. No. 3.1e-251;  
Matches 940; Conservative 1; Mismatches 145; Indels 4; Gaps 1;

|    |     |  |     |
|----|-----|--|-----|
| Qy | 101 | AGACATCTGCTGCTCAAGAAACAGACGAGGACATCAGCAGTCTCTATGAGATCCGGGA   | 160 |
| Db | 197 | AAACATCTGCTGCTGAAGAAACACACGGAGGACATCAGCAGCTCTACGAGATCCCGGA   | 256 |
| Qy | 161 | GAAGCTGGGCTCGGGTGCCTTCTCTGAGGTGATGCTGGCCCGAGAAAGGGGCTCTGCTCA | 220 |
| Db | 257 | GAGGCTCGGCTCGGGTGCCTTCTCCGAGGTGGTGTGCTGCCCGAGGCGGGGCTCCGCACA | 316 |
| Qy | 221 | TCTTGTGGCCCTCAAGTGCAATCCCAAGAAGCACTTCGGGGCAAGAGGCGCTGTGTGGA  | 280 |
| Db | 317 | CCTCGTGGCCCTCAAGTGCAATCCCAAGAAGGCGCTTCGGGGCAAGAGGCGCTGTGTGGA | 376 |
| Qy | 281 | GAATGAGATCGCGTACTTCGCAATCAGCCATCCCAACATTCGTGGCTCTGGAGGACT    | 340 |
| Db | 377 | GAACGAGATCGCAGTGTCCGTAGGATCAGTACCCCAACATCGTCTGTGGAGGATGT     | 436 |
| Qy | 341 | CCATGAGAGCTCTTCTCATCTCTACTTGGCCATGAGTGTGTACAGGTGGTGAATGTT    | 400 |
| Db | 437 | CCAGAGAGCCCTTCCCACTTACTTGGCCATGGAATGTTGACGGGTGGCGAGCTGTT     | 496 |
| Qy | 401 | TGACCCGCATATGAGCGGGGCTCTTACACAGAAGAGCAGCCAGCCACCTTGTAGGGCA   | 460 |
| Db | 497 | TGACCCGCATATGAGCGGGGCTCTTACACAGAAGAGGATGCCAGCCATCTGTGGGTCA   | 556 |
| Qy | 461 | GTCTCTGGGCTGTCTCTACCTTCAATAGCTGGGATCGTGACCGGACCTCAAGCC       | 520 |
| Db | 557 | GGTCTTTGGGCGCTCTCTACCTGACAGCGCTGGGATCGTGACCGGACCTCAAGCC      | 616 |

|    |      |   |      |
|----|------|---|------|
| Qy | 521  | TGAAAACCTCTCTATGCGCACACCTTTTGGAGACTCCAGATCATGTCTCTGACTTTGG      | 580  |
| Db | 617  | CGAAAACCTCTCTATGCGCACCGCCTTTGAGGACTCGAAGATCATGTCTCTGACTTTGG     | 676  |
| Qy | 581  | CCTGTCCAAATACAAGCTGCGCAACATGCTAGGCACAGCCTGTGGGACCCCGAGGATGT     | 640  |
| Db | 677  | ACTCTCCAAATCAAGCTGCGCAACATGCTAGGCACCGCCTGTGGGACCCCGAGGATGT      | 736  |
| Qy | 641  | GGCCCCAGAGCTCTCTGGAGCAGAAACCTTACGGGAAGCCGTAGATGTGGGCGCTTGGG     | 700  |
| Db | 737  | GGCCCCAGAGCTCTCTGGAGCAGAAACCTTACGGGAAGCCGTAGATGTGTGGGCGCTTGGG   | 796  |
| Qy | 701  | TGTCATCTCTACATCTCTGCTGTGGTACCCCGCCTTCTATGATGAGAGCGATCTCTGA      | 760  |
| Db | 797  | CGTCATCTCTACATCTCTGCTGTGGTACCCCGCCTTCTATGATGAGAGCGATCTCTGA      | 856  |
| Qy | 761  | ACTCTTCAGCCAGATCTCTGAGGCGCAGTATGATGTTGACTCCCGCTTTTGGGATGACAT    | 820  |
| Db | 857  | GCTCTTCAGCCAGATCTCTGAGGCGCAGTATGATGTTGACTTCCTTCTGGGATGACAT      | 916  |
| Qy | 821  | CTCAGAATCAGCCAAAGACTTTCATTCGCCACCTTCTGGAAACGTGATCCCCAGAGAGGTT   | 880  |
| Db | 917  | CTCAGAATCAGCCAAAGACTTTCATTCGCCACCTTCTGGAGCGAGACCTTCAGAAGAGGTT   | 976  |
| Qy | 881  | CACCTGCCAGCAGGCCCTTACAGCATCTTTGGATCTCTGGGGATGACACCTTCGATAGGGA   | 940  |
| Db | 977  | CACCTGCCAAGCGCCTTTCGGGACCTTTCGGATCTTTTGGGACACAGGCTTTGGCAGGGA    | 1036 |
| Qy | 941  | CATCTCTGGGTTCTGTCAGTCAGCAGATCCAGAGAGATTTTCCAGGAGCCACCTTGGAGCG   | 1000 |
| Db | 1037 | CATCTTAGGGTTTGTGTCAGTCAGCAGATCCCGAAGAACTTTGCTTGGACACACTGGAAAGCG | 1096 |
| Qy | 1001 | TGCATTCAATGCCACATCATCTCTAGCTACATCCGTAAGCTGGGACAAAGCCCGAGAGGG    | 1060 |
| Db | 1097 | AGCTTTCATGCGCACCTTGTCTCGGCCACATCCGGAAGCTGGGCGAGATCCAGAGGG       | 1156 |
| Qy | 1061 | TGAGGAGGCTCCAGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT   | 1120 |
| Db | 1157 | CGAGGGGGCTCTGAGCAGGCGATGAGGCGGACGACGACGACGACGACGACGACGACGACG    | 1216 |
| Qy | 1121 | GTCCCCAGTGGTGAACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG   | 1180 |
| Db | 1217 | GCCCCCAAGTGTGATGCCAGGAGATGCC----GAGGCCAAGTGTGANTGANTGANTGANTG   | 1272 |
| Qy | 1181 | TTTTTCTTTC  | 1190 |
| Db | 1273 | ATTNCTTNC   | 1282 |

RESULT 8  
US-10-948-518-9  
; Sequence 9, Application US/10948518  
; Publication No. US20050064492A1  
; GENERAL INFORMATION:  
; APPLICANT: FREDERIC J. DESAUVAGE  
; APPLICANT: GRETCHEN FRANTZ  
; APPLICANT: KENNETH J. HILLAN  
; APPLICANT: PAUL POLAKIS  
; APPLICANT: ANDREW POLSON  
; APPLICANT: VICTORIA SMITH  
; APPLICANT: SUSAN D. SPENCER  
; APPLICANT: THOMAS D. WU  
; APPLICANT: ZEMIN ZHANG  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
; TITLE OF INVENTION: TREATMENT OF TUMOR  
; FILE REFERENCE: P5026R1-US  
; CURRENT APPLICATION NUMBER: US/10/948,518  
; CURRENT FILING DATE: 2004-09-22  
; PRIOR APPLICATION NUMBER: US/10/643,795  
; PRIOR FILING DATE: 2003-08-19  
; PRIOR APPLICATION NUMBER: US 60/404,809  
; PRIOR FILING DATE: 2002-08-19  
; PRIOR APPLICATION NUMBER: US 60/405,645

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; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/413,192
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US 60/419,008
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/426,847
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/484,959
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 9
; LENGTH: 1282
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: 898, 1187, 1198, 1241, 1262, 1266, 1277, 1281
; OTHER INFORMATION: Unknown base
US-10-948-518-9

Query Match      54.3%; Score 844.4; DB 19; Length 1282;
Best Local Similarity 86.2%; Pred. No. 3.1e-251;
Matches 940; Conservative 1; Mismatches 145; Indels 4; Gaps 1;

QY 101 AGACATGCTGCTCTCAAGAAACAGACGAGGAGGACATCAGCAGTGTCTATGAGATCCGGGA 160
DB 197 AATCATGCTGCTCTGAAGAAACACACGAGGAGGACATCAGCAGGCTCTACGAGATCCGCGA 256
QY 161 GAAGCTGGGCTCGGGTGCCTTCTCTGAGGTGATGCTGGCCCGAGAAAGGGCTCTGTCTCA 220
DB 257 GAGGCTCGGCTCGGTGCTTCTCCGAGGTGTGTGCTGGCCCGAGAGGGGCTCCGACACA 316
QY 221 TCTTGTGGCCCTCAAGTGCATTCCTCAAGAAAGACATTCGCGGGCAAGAGGCCCTGTGTGA 280
DB 317 CCTCGTGGCCCTCAAGTGCATTCCTCAAGAAAGGCCCTCCGCGGGCAAGAGGCCCTGTGTGA 376
QY 281 GAATGAGATCGCGTACTTCGAGATTCAGCCATCCCAATTTGCTGCTCTGAGGACCT 340
DB 377 GAACGAGATCGCAGTGTCTGATGATCAGTACCCCAACATCGTGTCTGTGAGGATGT 436
QY 341 CCATGAGATGCTTCTCATCTTACTTGGCCATGGAGCTGGTAACAGGTGGTGAATGTT 400
DB 437 CCACGAGAGCCCTTCCACCTTCTACCTGGCCATGGAATGCTGACGGTGGCGAGCTGT 496
QY 401 TGACCGCATCATGAGCGGGCTCTTACACAGAGAGGACGCCAGCCACCTTGTAGGGCA 460
DB 497 TGACCGCATCATGAGCGGGCTCTTACACAGAGAGGATGCCAGCCATCTGGTGGTCA 556
QY 461 GGTCTTGGCGCTGCTCTTACCTTATAGCTGGGCATCGTCACCGGACCTCAAGCC 520
DB 557 GGTCTTGGCGCGTCTCTTACCTTATAGCTGGGCATCGTCACCGGACCTCAAGCC 616
QY 521 TGAACACCTCTCTATGCCACACCTTTTGAAGGACTCCAAAGATCATGTCTCTGACTTTGG 580
DB 617 CGAAACCTCTGTATGCCAGCGCTTTGAGGACTCGAAGATCATGTCTCTGACTTTGG 676
QY 581 CTGTCTCAAAATCAAGCTGGCAACATGCTAGGCACAGCTGTGGGACCCCAAGATATGT 640
DB 677 ACTCTCAAAATCCAGCTGGCAACATGCTAGGCACAGCTGTGGGACCCCTGGATATGT 736
QY 641 GSCCCAGAGCTCTTGAGCAGAAACCTACGGGAGGCGGTAGATGTGTGGGCCCTGGG 700
DB 737 GSCCCAGAGCTCTTGAGCAGAAACCTACGGGAGGCGGTAGATGTGTGGGCCCTGGG 796
QY 701 TGTCTATCTCTATCTCTGTGTGGGTACCCCTTCTATGATGAGAGCGATCTCTGA 760
DB 797 CGTCACTCTCTATCTCTGTGTGGGTACCCCTTCTACGAGAGAGCGACCTCTGA 856
QY 761 ACTCTCAGCAGATTCGAGGGCCAGCTATGATTTGATCTCCCTCTTTTGGATGACAT 820
DB 857 GCTCTTTCAGCAGATTCGAGGGCCAGCTATGATTTGATCTCTTCTTGGGATGACAT 916
QY 821 CTGAGATCAGCCAAAGACTTCTTCGCCACCTTCTGGAACGTGATCCCCAGAGAGGTT 880
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DB 917 CTCAGATCAGGCAAGACTTTATTGCGCACCTTCTTGGAGCGAGACTTTCAGAAGAGTT 976
QY 881 CACCTGCGCAGAGCGGCTTACAGATCTTTTGGATCTCTGGGATGAGACCTTCCATAGGGA 940
DB 977 CACCTGCCAACACAGGCTTTCGGGACCTTTTGGATCTTTTGGGACACAGGCTTTGGCAGGA 1036
QY 941 CATCTCTGGTCTGTCTGAGTGCAGATCCAGAGATTTTCCAGGACCCACTTGGAGCG 1000
DB 1037 CATCTTAGGGTTTGTGAGTGCAGATCCGGAAGAACTTTGCTTGGACACACTTGAAGCG 1096
QY 1001 TGCATTCAATGCGACATCATTTCTTACGTCACTCCCTAAGCTGGGCAAAAGCCAGAGGG 1060
DB 1097 AGCTTCAATGCGACCTTGTCTTGGCCACATCCGGAAGCTGGGCGAGATCCAGAGGG 1156
QY 1061 TGAGGAGGCTCCAGGACGTATGACCCGTATAGCCACCCAGGCTTGGGACTAGCCA 1120
DB 1157 CGAGGGGCTCTGAGCAGGCGATGSGCCGNCACAGCCACTTACGCTTGGGCTTGGGCA 1216
QY 1121 GTCCCCCAAGTGGTGAACACCAAGGTAGTCCCAAGGAAGGCCAAGTGGACTGACTCCCG 1180
DB 1217 GCGCCCAAGTGGTATGCCAGGNAGATGCC----GAGGCCAAGTGGANTGANTGCCAG 1272
QY 1181 TTTTCTTTTC 1190
DB 1273 ATTNTCTNC 1282

RESULT 9
US-10-656-598-15
; Sequence 15, Application US/10656598
; Publication No. US2004029232A1
; GENERAL INFORMATION:
; APPLICANT: DAVID P. DAVIS
; APPLICANT: FREDERIC J. DESAUVAGE
; APPLICANT: WILLIAM I. WOOD
; APPLICANT: ZEMIN ZHANG
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P1981R1P1-US
; CURRENT APPLICATION NUMBER: US/10/656,598
; CURRENT FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: US 60/410,166
; PRIOR FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 15
; LENGTH: 641
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Task 120 probe
US-10-656-598-15

Query Match      35.0%; Score 544; DB 18; Length 641;
Best Local Similarity 90.6%; Pred. No. 5e-158;
Matches 580; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 387 GGTGTGAACCTGTTTACCGCATCATGGAGCGGGCTCTTACATAGCTTGGGATCGTGCAC 446
DB 2 GGTGGCGAGCTGTTTACCGCATCATGGAGCGGGCTCTTACATAGCTTGGGATCGTGCAC 61
QY 447 CACCTTGTAGGCGAGTCTTGGCGCTGTCTCTTACCTTATAGCTTGGGATCGTGCAC 506
DB 62 CATCTGTGGTTCAGTCTTGGCGCGTCTCTTACCTGACAGCTTGGGATCGTGCAC 121
QY 507 CGGGACTCAAGCTGAAACCTCTCTATGCGACACCTTTTGGAGCTCCAAAGATCATG 566
DB 122 CGGGAAGCTCAAGCCCGAAGACCTCTCTGTATGCGACCGCTTTGAGGACTCGAAGATCATG 181
QY 567 GTCTCTGACTTTGGCTGTCCAAATAATACAGCTGGGCAACATGTAGGCAAGCTGTGGG 626
DB 182 GTCTCTGACTTTGGACTCTCCAAATCCAGGCTGGGAACATGTAGGCAAGCTGTGGG 241
```



QY 627 ACCCAGGATATGTGGCCCCAGAGCTCTCTGAGCAGAGAAACCCCTACGGGAAGGCGGTAGAT 686  
DB 242 ACCCTGGATATGTGGCCCCAGAGCTCTCTGAGCAGAGAAACCCCTACGGGAAGGCGGTAGAT 301  
QY 687 GTGTGGCCCTGGGTGTCTCTACATCTCTGCTGTGTGGTACCCCTCTCTATGAT 746  
DB 302 GTGTGGCCCTGGGTGTCTCTACATCTCTGCTGTGTGGTACCCCTCTCTATGAT 361  
QY 747 GAGAGCCATCTGAACCTCTTTCAGCCAGATCTTGTAGGGCCAGCTATGAGTTTGTATCCCTCC 806  
DB 362 GAGAGCCATCTGAACCTCTTTCAGCCAGATCTTGTAGGGCCAGCTATGAGTTTGTATCCCTCC 421  
QY 807 TTTTGGATGACATCTCAGATCAGCCAAAGACTTCTATTCGCCACCTTCTGGAACGTGAT 866  
DB 422 TTTTGGATGACATCTCAGATCAGCCAAAGACTTCTATTCGCCACCTTCTGGAACGTGAT 481  
QY 867 CCCAGAGAGGTTTCACTCTCCAGCGCCCTACAGCATCTTTGGATCTCTGGGGATGCA 926  
DB 482 CCCAGAGAGGTTTCACTCTCCAGCGCCCTTGGCCACCTTTGGATCTCTGGGGATGCA 541  
QY 927 GCCTTCGATAGGACATCTCTGGGTCTGTCTCAGTGAGCAGATCCAGAGAAATTTTGCACGG 986  
DB 542 GCCTTCGATAGGACATCTTAGGCTGTCTCAGTGAGCAGATCCAGAGAAATTTTGTCTCG 601  
QY 987 ACCACTGGAAGCGTGATTCATTCATGCGCACATCTCTAC 1026  
DB 602 ACACACTGGAAGCGAGCTTCAATGCCACCTCTCTCTGC 641

## RESULT 10

US-10-204-041-9  
; Sequence 9, Application US/10204041  
; Publication No. US2003017643A1  
; GENERAL INFORMATION:  
; APPLICANT: STEIN-GERLACH, MATTHIAS  
; APPLICANT: SALASIDIS, KONSTANTINOS  
; APPLICANT: BACHER, GERALD  
; APPLICANT: MULLER, STEFAN  
; TITLE OF INVENTION: Pyridylpyrimidine Derivatives as Effective Compounds Against Prio  
; TITLE OF INVENTION: Infections and Prio Diseases  
; FILE REFERENCE: AXM-007.1P US  
; CURRENT APPLICATION NUMBER: US/10/204,041  
; CURRENT FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: EP 01111858.5  
; PRIOR FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: PCT/EP02/05420  
; PRIOR FILING DATE: 2002-05-16  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 1480  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (104)..(106)  
; OTHER INFORMATION: n = a, c, g or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (118)..(118)  
; OTHER INFORMATION: n = a, c, g or t  
US-10-204-041-9

Query Match 32.2%; Score 500.8; DB 16; Length 1480;  
Best Local Similarity 72.0%; Pred. No. 1.8e-144;  
Matches 668; Conservative 0; Mismatches 257; Indels 3; Gaps 1;  
QY 119 GAAACACAGCAGGACATCAGCAGTGTCTATGATCCGGGAGAGCTGGGCTCGGTGC 178  
DB 177 GAGACGGCGAGACATTAAGACATCTACGACTTCCGAGATGTTCTGGGACGGGGC 236  
QY 179 CTTCTCTGAGGTGATGTGGCCCGAGGAGGGGCTCTGCTCATCTTGTGGCCCTCAAGTG 238

DB 237 CTTCTCGAGGTGATCTCTGCGAGAGATAGAGGACCGCAGAGCTGTGTGGCCATCAATG 296  
QY 239 CATTTCCCAAGAAAGCACTTCGGGCGAAGGAGGCGCTCTGTTGAGAAATCAGATCGCGGTACT 298  
DB 297 CATTTCCCAAGGCGCTTCGGAGGCGAAGGAGCAGCATGGAGAAATCAGATTCGTCTCT 356  
QY 299 TCGCAGATCAGCATCCCAACATTTGTGGCTCTGGAGGAGCTCCATGAGAGTCTCTTCTCA 358  
DB 357 GCACAAGATCAAGCACCACCAACATTTGAGCCCTGGATGACATCTATGAGAGTGGGGCCA 416  
QY 359 TCTCTACTTCTGGCCATGAGCTGTGTAACTGTGTGAGCTGTGTTGACCGCATCATGGAGCG 418  
DB 417 CTTCTACTCATCATGAGCTGTGTGCGGTGGGAGCTCTTTGACCGTATTTGGAATA 476  
QY 419 GGGCTCTCACAGAGAGGACCGCAGCCACCTTTGTAGGGCAGGTCTCTGGCGCTGTCTC 478  
DB 477 AGGCTTCTACAGCGAGCGGCGCAGCGCTCATCTTCCAGGTGCTGGATGCTGTGAA 536  
QY 479 CTACCTTCTAGGCTTGGGCTTCGTGCAACCGGACCTCAAGCTGTGAAACCTCTCTTATGC 538  
DB 537 ATACCTGATGACTGGGCAATTTGACACCGGATCTCAAGCCAGAGAAATCTGTGTACTA 596  
QY 539 CACACCTTTTGTAGGACTCCCAAGATCATGTCTCTGACTTTTGGCTGTCCAAATACAG- 597  
DB 597 CAGCTGGATGAAGACTCCAAATCATGATCTCCGACTTTGGCTCTCCAGATGGAGGA 656  
QY 598 --CTGGCAACATGCTAGGCACAGCTGTGGGACCCAGAGATATGTGGCCCGCAGAGCTCT 655  
DB 657 CCGGGCAGTGTCTCTCCACCGCTGTGAACTCCGGGATACGTGGCCCTGAAGTCTCT 716  
QY 656 GGAGCGAAACCTTACGGGAGCGGTAGATGTGTGGGCCCTGGGTGTCTATCTCTCAT 715  
DB 717 GGCCCGAGAGCCCTACAGCAAGCTGTGGATTTGCTGTCCATAGGTGTCTATCGCTACAT 776  
QY 716 CTTGCTGTGTGGTACCCCTCTTATGATGAGAGCGATCTTGAACCTCTTCAAGCAGAT 775  
DB 777 CTTGCTGTGTGGTACCCCTCTTATGAGAGAAATGATGCCAACTCTTTGAACAGAT 836  
QY 776 TCTGAGGCGCAGCTATGAGTTTCACTCCCTCTTGGGATGACATCTCAGAAATCAGCAA 835  
DB 837 TTTGAGGCGCAGTACGAGTTTCACTCTTACTTGGAGCAGCATCTTGAATCTGCGCA 896  
QY 836 AGACTTCATTTCGCCCTCTCTGGAACGTGATCCCGAAGAGGTTCACCTGCCAGAGCG 895  
DB 897 AGATTTTCATCCGCACTTGTATGAGAGGACCCAGAGAGAAAGATTACCTGTGAGCAGC 956  
QY 896 CTTACAGCATCTTTGGATCTCTGGGATGAGCTTCGATAGGAGATCTTGGGTCTGT 955  
DB 957 CTTGAGCAGCCCATGATTTGAGGAGATACAGCTCTAGATAAGAAATATCCACCAAGT 1016  
QY 956 CAGTGAGCAGATCCAGAGAAATTTTGGCAGGACCCACTGGAAGCGTGCATTTCAATGCCAC 1015  
DB 1017 GAGTGAGCAGATCAAGAGAACTTTGCCAAGCAGAGTGGAGCAAGCTTCAATGCCAC 1076  
QY 1016 ATCAATCTCTACATCCGTAAGCTG 1043  
DB 1077 GGCTGTGTGGCGCAGATGAGGAACTG 1104

## RESULT 11

US-10-305-720-1454  
; Sequence 1454, Application US/10305720  
; Publication No. US20040010136A1  
; GENERAL INFORMATION:  
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.  
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressi  
; FILE REFERENCE: PA-0002-1 CON  
; CURRENT APPLICATION NUMBER: US/10/305,720  
; CURRENT FILING DATE: 2002-11-26  
; PRIOR APPLICATION NUMBER: 09/016,434  
; PRIOR FILING DATE: 1998-01-30  
; NUMBER OF SEQ ID NOS: 1490  
; SOFTWARE: PERL Program

SEQ ID NO 1454  
LENGTH: 1480  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: GenBank ID No. US20040010136A1 g750789  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (1) ... (1480)  
OTHER INFORMATION: a, t, c, g, or other  
US-10-305-720-1454

Query Match 32.2%; Score 500.8; DB 17; Length 1480;  
Best Local Similarity 72.0%; Pred. No. 1.8e-144;  
Matches 668; Conservative 0; Mismatches 257; Indels 3; Gaps 1;

QY 119 GAAACAGACGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAGCTGGCTCGGGTGC 178  
DB 177 GAAGCAGGCGGAGACATTAAGACATCTACGACTTCCGAGATGTTCTGGGCACGGGGC 236  
QY 179 CTTCTCTGAGGTGATGCTGCCCCAGGAAAGGGCTCTGCTCATCTTTGTGGCCCTCAAGTG 238  
DB 237 CTTCTCGAGGTGATCTCTGCGAAGATTAAGAGCGCAGAAGCTGTGGCCATCAATG 296  
QY 239 CATTCCCAAGAAAGCACTTCGGGGCAAGGAGCCCTGGTGGAGAATGAGATCGGGTACT 298  
DB 297 CATTGCCAAGGAGGCCCTTGGAGGGCAAGGAGCAGCATGGAGAATGAGATTCTGTCT 356  
QY 299 TCCGAGAATCAGGCATCCCAACATTTGGGCTCTGGAGAGCTCCATGAGAGTCTTCTCA 358  
DB 357 GCACAGATCAAGACCCCAACATTTAGCCCTTGGATGACATCTATGAGAGTGGGGCCA 416  
QY 359 TCTCTACTTGGCCATGGAGCTGTAAACAGGTGGTGAACCTTTTGACCGCATCATGGAGC 418  
DB 417 CCTCTACTCATATGACGCTGTGTGCGGTGGGAGCTCTTTGACCGTATTGTGGAATA 476  
QY 419 GGGCTCTACAGAGAGAGACGCGCAGCACCTTTGTAGGCGAGTCTTGGCCGTCTCTC 478  
DB 477 AGGCTTTTACACGAGGCGGACGCCAGCCGCTCATCTCCAGGTGTGGATCTGTGA 536  
QY 479 CTACCTTTATAGCTGGGACCTGTGACACGGGACCTCAAGCTGAAACCTCTCTATGC 538  
DB 537 ATACCTGTGACTTGGGACCTGTGACACGGGATCTCAAGCAGAGATCTGTGTACTA 596  
QY 539 CACACCTTTTGGAGACTCCAAGATCATGTCTCTGACTTTTGGCTGTCCAAAATAACAAG- 597  
DB 597 CAGCTGGATGAAGACTCCAAATCATGATCTCGACTTTTGGCTCTCCAAAGATGGAG 656  
QY 598 --CTGGCAACATGTAGGCAAGCTGTGGACCCAGAGATATGTGGCCCCAGAGCTCT 655  
DB 657 CCGGGCAGTGTGTCTCCACCGCTGTGGAATCTCCGGGATACGTGGCCCTGAAATCT 716  
QY 656 GGAGCAGAAACCTTACGGGAGGCGTAGATGTGGGCCCTGGGTGTCTATCTCTACAT 715  
DB 717 GGCCAGAGCCCTTACAGAGGCTGTGGATGTGTGCTCATAGGTGTATCGCTTACAT 776  
QY 716 CTTGCTGTGGTACCCCTCTTATGATGAGAGCATCTTGAACCTTTACGCCAGAT 775  
DB 777 CTTGCTGTGGTATACCTCTCTTATGACGAGATGATGCCAACTCTTTGAACAGAT 836  
QY 776 TCTGAGGGCAGCTATGAGTTGATCTCCCTTTTGGGATGACATCTCAAGATCAGGCAA 835  
DB 837 TTTGAAGGGCAGTACGAGTTTGAATCTCTCTTACTTGGGAGCAGATCTCTGACTCTG 896  
QY 836 AGACTTCATTCGCCACCTCTTGAACGCTGATCCCAAGAGGTTACCTGCCAGCAGGC 895  
DB 897 AGATTTCATTCGGGCACTTGTAGAGAGGACCCAGAGAAAGATTACCTTGTAGCAGGC 956  
QY 896 CCTACAGCATCTTTGGATCTCTGCGGATGAGCCCTTCGATAGGAGACATCTCTGGTCTGT 955  
DB 957 CTTGACGACCCATGGATTGACGAGATACAGCTCTAGATAAGAAATATCCACCATCGGT 1016

QY 956 CAGTGAGCAGATCCAGAGAAATTTTCCAGGAGCCCACTGGAAGCGTGCAATTCATATGCCAC 1015  
DB 1017 GAGTGAGCAGATCAAGAGAACTTTTCCAGGAGCAGTGGAGCAAGCCTTCAATGCCAC 1076  
QY 1016 ATCAATCTCTACGTACATCCGTAAGCTG 1043  
DB 1077 GGTGTGTGGCGCACATGAGGAACTG 1104

RESULT 12  
US-10-649-400-5  
Sequence 5, Application US/10649400  
Publication No. US20040110198A1  
GENERAL INFORMATION:  
APPLICANT: Bunney Jr., William E.  
APPLICANT: Jones, Edward G.  
APPLICANT: Molnar, Margherita  
APPLICANT: The Board of Trustees of The Leland Stanford  
APPLICANT: Junior University  
TITLE OF INVENTION: Genes Involved in Neuropsychiatric Disorders  
FILE REFERENCE: 020885-000720US  
CURRENT APPLICATION NUMBER: US/10/649,400  
CURRENT FILING DATE: 2003-08-26  
PRIOR APPLICATION NUMBER: US 60/406,879  
PRIOR FILING DATE: 2002-08-28  
PRIOR APPLICATION NUMBER: US 60/451,306  
PRIOR FILING DATE: 2003-02-27  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 1501  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: calcium/calmodulin dependent protein kinase I  
OTHER INFORMATION: (CAMKI) cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (179)..(1291)  
OTHER INFORMATION: CAMKI  
US-10-649-400-5

Query Match 32.2%; Score 500.8; DB 18; Length 1501;  
Best Local Similarity 72.0%; Pred. No. 1.8e-144;  
Matches 668; Conservative 0; Mismatches 257; Indels 3; Gaps 1;

QY 119 GAAACAGACGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAGCTGGCTCGGGTGC 178  
DB 208 GAAGCAGGCGGAGACATTAAGACATCTACGACTTCCGAGATGTTCTGGGCACGGGGC 267  
QY 179 CTTCTCTGAGGTGATGCTGTGGCCAGGAAAGGGCTCTGCTCATCTTGTGGCCCTCAAGTG 238  
DB 268 CTTCTCGAGGTGATCTCTGCGAAGATAAGAGGACGCGAGAAGCTGGTGCCATCAATG 327  
QY 239 CATTCCCAAGAAAGCACTTCGGGGCAAGGAGCCCTGGTGGAGATCAGATCGGGTACT 298  
DB 328 CATTGCCAAGGAGCCCTTGGAGGCGAAGGAGCAGCATGGAGATGCTGTCTCT 387  
QY 299 TCGCAGAATCAGCCATCCCAACATTTGGCTCTGGAGGACGTCCATGAGAGTCTCTCA 358  
DB 388 GCACAAAGATCAAGCACCCCAACATTTAGCCCTGGATGACATCTATGAGAGTGGGGCCA 447  
QY 359 TCTCTACTTGGCCATGAGCTGTAAACAGTGTGTAACCTTTTGACCGCATCATGGAGCG 418  
DB 448 CCTCTACTCATATGACGCTGTGTGGGTGGGAGCTCTTTGACCTATTGTGGAATA 507  
QY 419 GGGCTCTCACACAGAGAAGGACCGCCAGCCACCTTGTAGGCGAGTCTCTGGCGCTGCTC 478  
DB 508 AGGCTTCTACACGAGGCGGAGCCAGCCCTCATCTTCCAGGTGTGATGCTGTGAA 567  
QY 479 CTACCTTCTATGAGCTGGGCATCGTGCAACCGGACCTCAAGCCTGAAACCTCTCTATGC 538  
DB 568 ATACCTGCATGACCTGGGCATTTGACACCGGGATCTCAAGCCGAGATCTGCTGTACTA 627





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Qy 654 CTGAGCAGAAACCTACGGGAAGCCGTAGATGTGGGCCCTGGGTGTCATCTCTAC 713
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 577 CTGCCCAGAAACCTTACAGCAAGCCGTTGACTGTGTGGTCCATCGGAGTGATGCTAC 636
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 714 ATCTGTGTGTGGTACCCCTCTATGATGAGAGCGATCCTGAACCTCTTCAGCCAG 773
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 637 ATCTGTCTGTGGCTACCCCTCTTTTATGATGAAAATGACTCCAAGCTCTTTGAGCAG 696
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 774 ATCTGAGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACATCTCAGAATCAGCC 833
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 697 ATCTCAAGGGGAATATGAGTTTGACTCTCCCTACTGGGATGACATCTCGACTCTGCA 756
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 834 AAGACTTCAATTCGCCACCTTCTGGAACGTGATCCCCAGAAAGAGTTTCACTGCCAGCAG 893
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 757 AAGACTTCAATTCGGAACCTGATGGAGAAGGACCCGGAATAAAGATACAGGTGTGAGCAG 816
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 894 GCCCTACAGCATCTTTGGATCTCTGGGATGCGAGCCTTCGATAGGGACATCCTGGTTCT 953
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 817 GCAGCTCGGACCCCATGGTGTGTCACAGCCCTCAACAAAAACATCCAGAGTCC 876
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 954 GTCAGTGAGCAGATCCAGAAAGATTTTGCAGGACCCCACTGGAAAGCGTGATTCATGCC 1013
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 877 GTCAGGCCCAGATCCGAAAAACTTTGCCAAGAGCAATGGAGACAAGCATTTAATGCC 936
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1014 ACATCATTCCTACGTACATCCCGTAAGCT 1042
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 937 ACGGCCGTCGTGAGACATATGAGAAAACT 965
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Search completed: June 6, 2005, 11:44:13  
Job time : 6844 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 6, 2005, 08:23:56 ; Search time 52 Seconds  
(without alignments)  
5750.802 Million cell updates/sec

Title: US-10-032-254A-1

Perfect score: 2872  
Sequence: 1 gttcgagtcctccactc.....caaaaaaaaaaaaaaa 1554

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USFTO\_spool\_P/US10032254/runat\_02062005\_131019\_3607/app\_query.fasta\_1.1735  
-DB=PIR\_79 -QMT=fastan -SUFFIX=pr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=Bites -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10032254 @CGN 1.1 41 @runat\_02062005\_131019\_3607 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR\_79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID    | Description        |
|------------|--------|-------------|--------|----------|--------------------|
| 1          | 1188.5 | 41.4        | 374    | 1 S50193 | Ca2+/calmodulin-de |
| 2          | 1184.5 | 41.2        | 370    | 1 S57347 | Ca2+/calmodulin-de |
| 3          | 1010.5 | 35.2        | 348    | 2 T73321 | Ca2+/calmodulin-de |
| 4          | 874.5  | 30.4        | 310    | 2 B88640 | protein X07A9.2 [i |
| 5          | 730    | 25.4        | 473    | 1 A53036 | Ca2+/calmodulin-de |
| 6          | 724.5  | 25.2        | 474    | 1 TVRTC4 | Ca2+/calmodulin-de |
| 7          | 722.5  | 25.2        | 502    | 2 I52637 | Ca2+/calmodulin-de |
| 8          | 719    | 25.0        | 469    | 1 S17656 | Ca2+/calmodulin-de |
| 9          | 717    | 25.0        | 504    | 2 I56542 | calmodulin-binding |
| 10         | 705    | 24.5        | 421    | 2 T30814 | calmodulin-binding |
| 11         | 695    | 24.2        | 301    | 1 A40811 | myosin-light-chain |
| 12         | 647    | 22.5        | 414    | 2 A03233 | Ca2+/calmodulin-de |
| 13         | 638    | 22.2        | 335    | 2 T50230 | calmodulin kinase  |
| 14         | 611.5  | 21.3        | 509    | 2 B44412 | calmodulin-depende |

|    |       |      |     |          |                    |
|----|-------|------|-----|----------|--------------------|
| 15 | 611.5 | 21.3 | 516 | 1 JU0270 | Ca2+/calmodulin-de |
| 16 | 611.5 | 21.3 | 530 | 2 D44412 | Ca2+/calmodulin-de |
| 17 | 594.5 | 20.7 | 478 | 1 A30355 | Ca2+/calmodulin-de |
| 18 | 593.5 | 20.7 | 589 | 2 S68470 | Ca2+/calmodulin-de |
| 19 | 591.5 | 20.6 | 518 | 1 S43845 | Ca2+/calmodulin-de |
| 20 | 591   | 20.6 | 508 | 1 A43713 | calcium-dependent  |
| 21 | 589.5 | 20.5 | 478 | 1 S04365 | Ca2+/calmodulin-de |
| 22 | 589   | 20.5 | 527 | 1 A31908 | Ca2+/calmodulin-de |
| 23 | 588   | 20.5 | 490 | 2 T08873 | calcium-dependent  |
| 24 | 587   | 20.4 | 610 | 1 A49082 | calcium-dependent  |
| 25 | 586   | 20.4 | 520 | 2 C84774 | probable calcium-d |
| 26 | 586   | 20.4 | 531 | 1 T02593 | calcium-dependent  |
| 27 | 584.5 | 20.4 | 639 | 1 T02784 | calcium-dependent  |
| 28 | 584   | 20.3 | 518 | 1 B46619 | Ca2+/calmodulin-de |
| 29 | 584   | 20.3 | 556 | 2 JC5636 | Ca2+/calmodulin-de |
| 30 | 582   | 20.3 | 446 | 2 A40896 | Ca2+/calmodulin-de |
| 31 | 582   | 20.3 | 513 | 1 T02259 | calcium-dependent  |
| 32 | 581   | 20.2 | 504 | 2 T38226 | probable serine-th |
| 33 | 580.5 | 20.2 | 708 | 2 T23616 | hypothetical prote |
| 34 | 580   | 20.2 | 533 | 1 A34366 | Ca2+/calmodulin-de |
| 35 | 580   | 20.2 | 580 | 2 T40939 | probable Ca-calmod |
| 36 | 578.5 | 20.1 | 554 | 2 T05476 | calcium-dependent  |
| 37 | 578   | 20.1 | 490 | 1 S71776 | calcium-dependent  |
| 38 | 578   | 20.1 | 583 | 2 H84810 | probable calcium-d |
| 39 | 576   | 20.1 | 542 | 1 A45025 | Ca2+/calmodulin-de |
| 40 | 574   | 20.0 | 495 | 1 S46284 | calcium-dependent  |
| 41 | 574   | 20.0 | 501 | 2 G85097 | hypothetical prote |
| 42 | 574   | 20.0 | 542 | 1 A26464 | Ca2+/calmodulin-de |
| 43 | 570.5 | 19.9 | 553 | 1 T02139 | calcium-dependent  |
| 44 | 570   | 19.8 | 447 | 2 B40896 | Ca2+/calmodulin-de |
| 45 | 569.5 | 19.8 | 531 | 2 D85059 | probable calcium d |

#### ALIGNMENTS

##### RESULT 1

S50193  
N:Alternate names: CAMKI  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: S50193; A49682; A46038  
R:Cho, F.S.; Phillips, K.S.; Bogucki, B.; Weaver, T.E.  
Biochim. Biophys. Acta 1224, 156-160, 1994  
A:Title: Characterization of a rat cDNA clone encoding calcium/calmodulin-dependent protein kinase  
A:Reference number: S50193; MUID:95035115; PMID:7948038  
A:Accession: S50193  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-374 <CHO>  
A:Cross-references: UNIPROT:O63450; EMBL:L26288; NID:9439613; PIDN:AAA66944.1; PID:9439613  
R:Picciotto, M.R.; Czernik, A.J.; Nairn, A.C.  
J. Biol. Chem. 268, 26512-26521, 1993  
A:Title: Calcium/calmodulin-dependent protein kinase I. cDNA cloning and identification  
A:Reference number: A49682; MUID:94075341; PMID:8253780  
A:Accession: A49682  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-111, 'G', 113-117, 'R', 119-308, 'R', 310-322, 'HQPQ', 327, 'T', 329, 'TDS' <PIC>  
A:Cross-references: GB:L24907; NID:9406112; PIDN:AAA19670.1; PID:9406113  
R:Mochizuki, H.; Ito, T.; Hidaka, H.  
J. Biol. Chem. 268, 9143-9147, 1993  
A:Title: Purification and characterization of Ca2+/calmodulin-dependent protein kinase  
A:Reference number: A46038; MUID:93232082; PMID:8386178  
A:Accession: A46038  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 12-36, 'T' <MOC>  
A:Experimental source: cerebrium  
A>Note: sequence extracted from NCBI backbone (NCBIP:129927)  
C:Superfamily: Ca2+/calmodulin-dependent protein kinase I; protein kinase homology  
C:Keywords: ATP; autophosphorylation; calmodulin binding; phosphoprotein; phosphotransferase  
F:18-276/Domain: protein kinase homology <KIN>

F;26-34/Region: protein kinase ATP-binding motif  
F;293-299/Region: autoinhibitory  
F;302-314/Region: calmodulin binding  
F;177/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

Alignment Scores:  
Pred. No.: 9,33e-45 Length: 374  
Score: 1188.50 Matches: 221  
Percent Similarity: 85.53% Conservative: 51  
Best Local Similarity: 69.50% Mismatches: 43  
Query Match: 41.38% Indels: 3  
DB: 1 Gaps: 2

US-10-032-254A-1 (1-1554) x S50193 (1-374)

QY 120 AAACAGACGGAGACATCAGACGTGCTATGAGATCCGGGAGAGCTGGCTCGGGTGC 179  
Db 11 LysGlnAlaGluAspIleArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla 30  
QY 180 TTCTCTGAGTGATGCTGGCCAGGAAGGGCTCTGCTCATCTTTGGCCCTCAAGTGC 239  
Db 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50  
QY 240 ATTCCCAAGAAACACTTCGGGCAAGAGCGCCCTGGTGAGAAATGAGATCGCGGTACTT 299  
Db 51 IleAlaLysLysAlaLeuGluGlyLysGluGlySerMetGluAsnGluIleAlaValLeu 70  
QY 300 CGCAGAATCAGCCATCCCAATTTGGCTCTCGGAGGACCTCCATGAGAGTCTTCTCAT 359  
Db 71 HisLysIleLysHisProAsnIleValAlaLeuAspAspIleTyrGluSerGlyGlyHis 90  
QY 360 CTCTACTTGGCCATGAGCTGGTAAACAGGTGGTGAAGTCTTACCGCATCATGAGCGG 419  
Db 91 LeuTyrLeuIleMetGlnLeuValSerGlyGlyLeuPheAspArgIleValGluLys 110  
QY 420 GGCTCTTACACAGAGAGGACGCCAGCCACTTGTAGGCGAGTCTTGGCGTGTCTCC 479  
Db 111 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130  
QY 480 TACCTTCATAGCTGGGCATCTGTGCACCGGACCTCAAGCGCTGAACCTCAATGCTATGCC 539  
Db 131 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuLeuTyrTyr 150  
QY 540 ACACCTTTTGGAGTCTCAAGATCATGCTGTAGGCGAGTCTTGGCGTGTCTCC --- 596  
Db 151 SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp 170  
QY 597 GCTGGCAACATGCTAGGCACAGCTGTGGACCCAGGATATGTGGCCCGCAGAGCTCTG 656  
Db 171 ProGlySerValLeuSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeu 190  
QY 657 GAGCAGAAACCTACCGGAAGCGGTAGATGTGTGGCCCTGGGTGTCTCTCTCATC 716  
Db 191 AlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyrIle 210  
QY 717 CTGCTGTGTGGTACCCCTTCTATGATGAGAGCGCATCCTGAACTTCTTACGCCAGATT 776  
Db 211 LeuLeuCysGlyTyrProProPheTyrAspGluAsnAspAlaLysLeuPheGluGlnIle 230  
QY 777 CTGAGGCCAGCTATGATAGTTTGACTCCCTTTTGGGATGACATCTCAGAAATCAGCCAAA 836  
Db 231 LeuLysAlaGluTyrGluPheAspSerProTyrTrpAspAspIleSerAspSerAlaLys 250  
QY 837 GACTTCATTCGCCACTTCTGGACGTATCCCGAAGAGGTTTCACTTCCGACGAGGCC 896  
Db 251 AspPheIleArgHisLeuMetGluLysAspProGluLysArgPheThrCysGluGlnAla 270  
QY 897 CTACAGCATCTTGGATCTCTGGGGATGCGAGCTTCGATAGGACATCTTGGGTCTGTG 956  
Db 271 LeuGlnHisProTrpIleAlaGlyAspThrAlaLeuAspLysAsnIleHisGlnSerVal 290  
QY 957 AGTGAGCAGATCCAGAGAATTTTGGCCAGGACCCACTTGGAGCGTGCATTTCAATGCCACA 1016

Db 291 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 310  
QY 1017 TCATTCCTACGTACATCCGTAG-----CTGGGACAAAGCCAGAGGGTGAG 1064  
Db 311 AlaValValArgHisMetArgLysLeuGlnLeuGlyThrSerGlnGluGlyGln 328

RESULT 2  
S57347  
Cat+/calmodulin-dependent protein kinase (EC 2.7.1.123) I - human  
N;Alternate names: CaMKI  
C;Species: Homo sapiens (man)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: S57347  
R;Haribabu, B.; Hook, S.S.; Selbert, M.A.; Goldstein, E.G.; Tomhave, E.D.; Edelman, A.M.  
EMBO J. 14, 3679-3686, 1995  
A;Title: Human calmodulin dependent protein kinase I: cDNA cloning, domain structure, and expression.  
A;Reference number: S57347; MUID:95369239; PMID:7641687  
A;Accession: S57347  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-370 <HAR>  
A;Cross-references: UNIPROT:Q14012; EMBL:L41816; NID:g790789; PIDN:AAA99458.1; PID:g790789

C;Genetics:  
A;Gene: GDB:CAMK1  
A;Cross-references: GDB:642249  
C;Superfamily: Cat+/calmodulin-dependent protein kinase I; protein kinase homology  
C;Keywords: ATP; autophosphorylation; calmodulin binding; phosphoprotein; phosphotransferase; protein kinase  
F;18-276/Domain: protein kinase homology <KIN>  
F;26-34/Region: protein kinase ATP-binding motif  
F;293-299/Region: autoinhibitory  
F;302-314/Region: calmodulin binding  
F;177/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

Alignment Scores:  
Pred. No.: 1.39e-44 Length: 370  
Score: 1184.50 Matches: 220  
Percent Similarity: 85.53% Conservative: 52  
Best Local Similarity: 69.18% Mismatches: 43  
Query Match: 41.24% Indels: 3  
DB: 1 Gaps: 2

US-10-032-254A-1 (1-1554) x S57347 (1-370)

QY 120 AAACAGACGGAGACATCAGACGTGCTATGAGATCCGGGAGAGCTGGCTCGGGTGC 179  
Db 11 LysGlnAlaGluAspIleArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla 30  
QY 180 TTCTCTGAGTGATGCTGGCCAGGAAGGGCTCTGCTCATCTTGTGGCCCTCAAGTGC 239  
Db 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50  
QY 240 ATTCCCAAGAAACACTTCGGGCAAGAGCGCCCTGGTGAGAAATGAGATCGCGGTACTT 299  
Db 51 IleAlaLysLysAlaLeuGluGlyLysGluGlySerMetGluAsnGluIleAlaValLeu 70  
QY 300 CGCAGAATCAGCCATCCCAACATTTGGCTCTCGGAGGACCTCCATGAGAGTCTTCTCAT 359  
Db 71 HisLysIleLysHisProAsnIleValAlaLeuAspAspIleTyrGluSerGlyGlyHis 90  
QY 360 CTCTACTTGGCCATGAGCTGGTAAACAGGTGGTGAAGTCTTTCACCGCATCATGAGCGG 419  
Db 91 LeuTyrLeuIleMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGluLys 110  
QY 420 GGCTCTTACACAGAGAGGACGCCAGCCACTTTGTAGGCGAGGTCCTTGGCGTGTCTCC 479  
Db 111 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130  
QY 480 TACCTTCATAGCTGGGCATCTGTGCACCGGACCTCAAGCGCTGAACCTCTCTATGCC 539  
Db 131 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuLeuTyrTyr 150  
QY 540 ACACCTTTTGGAGTCTCAAGATCATGCTGTAGGCGAGTCTTGGCGTGTCTCCAAAATACAA --- 596







Db 66 LysGlyThrGlnLysProTyrAlaLeuLysValLeuLysLysThrVal-----Asp 82  
QY 267 GAGGCCCTGGTGGAGAAATGAGATCGCGGTACTTTCGAGAAATCAGCAGCATCCCAACATGTGTG 326  
Db 83 LysLysIleValargThrGluIleGlyValLeuLeuArgLeuSerHisProAsnIleIle 102  
QY 327 GCTCTGAGGACCTGCATGAGAGTCCCTTCTCATCTCTACTCTACTCTGAGGAGTGGTAACA 386  
Db 103 LysLeuLysGluIlePheGluThrProThrGluIleSerLeuValLeuGluLeuValThr 122  
QY 387 GGTGGTGAACCTGTTGACCCCATCATCGAGCGGGCTCTCTACACAGAGAGGAGCGCAGC 446  
Db 123 GlyGlyGluLeuPheAspArgIleValGluIleGlyTyrTyrSerGluArgAspAlaAla 142  
QY 447 CACCTTGTAGGCGAGTCCCTTGGCGTGTCTCTACCTCATGACCTGGGCATCTGTGCAC 506  
Db 143 AspAlaValLysGlnIleLeuGluAlaValAlaTyrLeuHisGluAsnGlyIleValHis 162  
QY 507 CGGAGCTCAAGCTGAAACCTCTCTATGCGACACCTTTTGGAGGACTCCAAGATCATG 566  
Db 163 ArgAspLeuLysProGluAsnLeuLeuTyrAlaThrProAlaProAspAlaProLeuLys 182  
QY 567 GTCTCTGACCTTGGCCTGTCCAAATACAAGCTGGCAACATGCTA---GGCAGACCTGT 623  
Db 183 IleAlaAspPheGlyLeuSerLysIleValGluHisGlnValLeuMetLysThrValCys 202  
QY 624 GGGACCCAGCATATGTGGCCCGCCAGAGCTCTCTGAGCAGAGAAACCTACGGGAAGCCGTA 683  
Db 203 GlyThrProGlyTyrCysAlaProGluIleLeuArgGlyCysAlaTyrGlyProGluVal 222  
QY 684 GATGTGTGGCCCTGGGTGTCTCTCATCTCTGCTGTGTGGGTATCCGCCCTTCTCTAT 743  
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QY 744 GATGAG---AGCCATCTGTAACCTTCAGCCAGATCTCTGAGGCGCCACTATGATTTGAC 800  
Db 243 AspGluArgGlyAspGlnPheMetPheArgIleLeuAsnCysGluTyrTyrPheIle 262  
QY 801 TCCCCCTTTGGGATGACATCTCAGAAATCAGCAAGACATCTTCCTGCCACCTCTCGAA 860  
Db 263 SerProTrpTrpAspGluValSerLeuAsnAlaLysAspLeuValArgLysLeuIleVal 282  
QY 861 CGTGATCCCCAGAGGTTTCACTGCGCAGCAGCCCTACAGCATCTTTTGGATCTCTGGG 920  
Db 283 LeuAspProLysLysArgLeuThrThrPheGlnAlaLeuGlnHisProTrpValThrGly 302  
QY 921 GATGAGCCTTCATAGGAGCATCTCGGGTCTGTCTAGTGAGCAGATCCAGAGAATTTT 980  
Db 303 LysAlaAla---AsnPheValHisMetAspThrAlaGlnLysLysLeuGlnGluPheAsn 321  
QY 981 GCCAGGACCCACTGGAGCGTGCATTCATCAATGCCACATCATCTCTACGTCCATCCGTAAG 1040  
Db 322 AlaArgLysLysLysAlaAlaValLysAlaVal----- 333  
QY 1041 CTGGGCAAAACCCAGAGGGTGGAGGCGCTCCAGGCGAGTGTATGACCCCGTCATAGCCAC 1100  
Db 334 ValAlaSerSerArgLeuGlySerAlaSerSerHisGlySerIleGlnGluSerHis 353  
RESULT 6  
TVR4  
N;Alternate names: Ca2+/calmodulin-dependent protein kinase Gr  
N;Contains: calspermin  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 31-Mar-1993 #sequence, revision 31-Mar-1993 #text, change 09-Jul-2004  
C;Accession: A41103; A32865; A41250; A32035; A60255; I53706  
R;Ohmstede, C.A.; Bland, M.M.; Merrill, B.M.; Sahyoun, N.  
Proc. Natl. Acad. Sci. U.S.A. 88, 5784-5788, 1991  
A;Title: Relationship of genes encoding Ca(2+)/calmodulin-dependent protein kinase Gr and  
A;Reference number: A41103; MUID:91288548; PMID:1648230  
A;Accession: A41103  
A;Molecule type: DNA  
A;Residues: 47-141, 'NE', 144-474 <OH1>

A;Cross-references: UNIPROT:P13234; GB:M74488; NID:G203219; PIDN:AAA40845.1; PID:G20322  
A;Note: this sequence has been revised in reference A41237  
A;Note: part of this sequence was confirmed by sequencing of cDNA to mRNA  
R;Ohmstede, C.A.; Bland, M.M.; Merrill, B.M.; Sahyoun, N.  
Proc. Natl. Acad. Sci. U.S.A. 88, 9375, 1991  
A;Reference number: A41237  
A;Accession: A41237  
A;Molecule type: DNA  
A;Residues: 142-143 <OH2>  
A;Cross-references: GB:M63334  
A;Note: this is a revision to the sequence from reference A41103  
R;Ohmstede, C.A.; Jensen, K.F.; Sahyoun, N.E.  
J. Biol. Chem. 264, 5866-5875, 1989  
A;Title: Ca(2+)/calmodulin-dependent protein kinase enriched in cerebellar granule cell  
A;Reference number: A32865; MUID:89174647; PMID:2538431  
A;Accession: A32865  
A;Molecule type: mRNA  
A;Residues: 250-474 <OH3>  
A;Cross-references: GB:J04600; NID:G206172; PIDN:AAA41867.1; PID:G206173  
R;Means, A.R.; Cruzalegui, F.; LeMagueresse, B.; Needleman, D.S.; Slaughter, G.R.; Ono,  
Mol. Cell. Biol. 11, 3960-3971, 1991  
A;Title: A novel Ca(2+)/calmodulin-dependent protein kinase and a male germ cell-specific  
A;Reference number: A41250; MUID:91304387; PMID:1649385  
A;Accession: A41250  
A;Molecule type: mRNA  
A;Residues: 1-371, 'M', 373-408, 'Q', 410-474 <MEA>  
A;Cross-references: GB:M64757  
R;Ono, T.; Slaughter, G.R.; Cook, R.G.; Means, A.R.  
J. Biol. Chem. 264, 2081-2087, 1989  
A;Title: Molecular cloning sequence and distribution of rat calspermin, a high affinity  
A;Reference number: A32035; MUID:89132272; PMID:2914893  
A;Accession: A32035  
A;Molecule type: mRNA  
A;Residues: 306-371, 'M', 373-474 <ON1>  
A;Cross-references: GB:J04446; NID:G203642; PIDN:AAA40990.1; PID:G203643  
R;Ono, T.; Means, A.R.  
Adv. Exp. Med. Biol. 255, 263-268, 1989  
A;Title: Calspermin is a testis specific calmodulin-binding protein closely related to  
A;Reference number: A60255; MUID:90144189; PMID:2618865  
A;Accession: A60255  
A;Molecule type: protein  
A;Residues: 335-363 <ON2>  
A;Note: the amino end of calspermin was blocked  
R;Bland, M.M.  
Gene 137, 351-352, 1993  
A;Title: Identification of alternate 5' untranslated regions in the gene encoding Ca2+/  
A;Reference number: I53706; MUID:94131312; PMID:8299971  
A;Accession: I53706  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-37 <RSS>  
A;Cross-references: GB:I16999; NID:G310086; PIDN:AAA17443.1; PID:G310087  
C;Comment: Ca2+/calmodulin-dependent protein kinase IV is enriched in cerebellar granu-  
und in sperm cells.  
C;Superfamily: Ca2+/calmodulin-dependent protein kinase; protein kinase homology  
C;Keywords: alternative splicing; ATP; calmodulin binding; phosphotransferase; serine/t  
F;40-296/Domain: protein kinase homology <KIN>  
F;48-57/Region: protein kinase ATP-binding motif  
F;306-474/Product: calspermin #status predicted <CSP>  
F;318-337/Region: calmodulin binding #status predicted  
F;71/Active site: Lys #status predicted  
Alignment Scores:  
Pred. No.: 1.09e-24 Length: 474  
Percent: 724.50 Matches: 156  
Score: 62.88% Conservative: 71  
Best Local Similarity: 43.21% Mismatches: 118  
Query Match: 25.23% Indels: 16  
DB: 1 Gaps: 6  
US-10-032-254A-1 (1-1554) x TVR4 (1-474)  
QY 96 GTCGACATGCTGCTGCTCAAGAAACAGCGGAGGACATCAGCTGTCTATGAGATC 155





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Db 321 LysLeuLysAlaIaValLysAlaVal-----ValAlaSer 332
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Db 333 SerArgLeuGlySerAlaSerSerHisThrSerIleGlnGluAsnHis-LysAla-- 351
QY 1110 GGGACTAGCAGTCCCGCCCAAGTGGTGAACACCAAGGTAGATGCCAAGAA 1158
Db 352 ----SerSerAspProProSerThrGlnAspAlaLysAspSerThrAsp 366

RESULT 9
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Aug-2004
R;Godbout, M.; Erlander, M.G.; Hasel, K.W.; Danielson, P.E.; Wong, K.K.; Battenberg, E.L
J. Neurosci. 14, 1-13, 1994
A;Title: I65: a calmodulin-binding, vesicle-associated, protein kinase-like protein enri
A;Reference number: I56542; MUID:94110847; PMID:8283228
A;Accession: I56542
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-504 <RES>
A;Cross-references: UNIPROT:Q63092; GB:I22557; NID:G349074; PIDN:AAA16633.1; PID:G349075
C;Superfamily: protein kinase homology
C;Keywords: calmodulin binding
F;22-286/Domain: protein kinase homology <KIN>

Alignment Scores:
Pred. No.: 2,28e-24 Length: 504
Score: 717.00 Matches: 154
Percent Similarity: 59.18% Conservative: 78
Best Local Similarity: 39.29% Mismatches: 131
Query Match: 24.97% Indels: 29
DB: 2 Gaps: 5

US-10-032-254A-1 (1-1554) x I56542 (1-504)
QY 123 CAGACGAGGACATCAGCAGTGTCTATGAGATCCGGAGAAGCTGGGCTCGGCTGCCTC 182
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QY 183 TCTGAGTGATGTGGCCAGGAAGGGCTCTGCTCATCTTGTGGCCCTCAAGTGCATT 242
Db 36 CysGluIlePheArgAlaLysAspLysThrGlyLysLeuHisThrCysLysLysPhe 55
QY 243 CCCAAGAAAGCACTTCGGGGCAGGAGCCCTGCTGGAGATGAGATCGCGTACTCGC 302
Db 56 GlnLysArgAspGlyArgLysValArgLysAlaAlaLysAsnGluIleGlyIleLeuLys 75
QY 303 AGAATCAGCATCCCAACATTGTGGCTCTGGAGGAGCTCCATGAGATGCTTCTCATCTC 362
Db 76 MetValLysHisProAsnIleLeuGlnLeuValAspValPheValThrArgLysGluTyr 95
QY 363 TACTTGCCATGAGCTGGTAACAGTGGTGAACATGTTTGACCGCATCATGAGCGGGC 422
Db 96 PheIlePheLeuGluLeuAlaThrGlyArgGluValPheAspTrpIleLeuAspGlnGly 115
QY 423 TCCTACACAGAGAGGAGCCAGCCACTTGTAGGGCAGGCTCTTGGCGGTGCTCTCTAC 482
Db 116 TyrTyrSerGluArgAspThrSerAsnValValArgGlnValLeuGluAlaValAlaTyr 135
QY 483 CTTTCATAGCTGGGCATCTGGCACCGGAGCTCAAGCTGAAACCTCTCTATGCCACA 542
Db 136 LeuHisSerLeuLysIleValHisArgAsnLeuLysLeuGluAsnLeuValTyrTyrAsn 155
QY 543 CTTTGTGAGACTCCAGATCATGGTCTCTGACCTTTGGCTGTGCCAAATACAAAGCTGGC 602
Db 156 ArgLeuLysAsnSerLysIleValIleSerAspPheHisLeuAlaLysLeuGluAsnGly 175
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Db 176 ----LeuIleLysGluProCysGlyThrProGluTyrLeuAlaProGluValValGlyArg 194
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Db 195 GlnArgTyrGlyArgProValAspCysTrpAlaIleGlyValIleMetTyrIleLeuLeu 214
QY 723 TGTGGGTACCCCGCTTCTATGATGAG-----ACGGATCCT 758
Db 215 SerGlyAsnProProPheTyrGluGluValGluGluAspAspTyrGluAsnHisAspLys 234
QY 759 GAACTCTTCAGCCAGCATCTTGAGGGCCAGCTATGAGTTTGACTCCCGCTTTTGGGATGAC 818
Db 235 AsnLeuPheArgLysIleLeuAlaGlyAspTyrGluPheAspSerProTyrTrpAspAsp 254
QY 819 ATCTCAGAAATCAGCCAAAGACTTCATTCGCCACCTTCTGGAAAGTATCCCCAGAAAGG 878
Db 255 IleSerGlnAlaAlaLysAspLeuValThrArgLeuMetGluValGluGlnAspGlnArg 274
QY 879 TTCACCTGCCAGCAGCCCTACAGCATCTTGGATCTCTGGGGATGCGAGCTTCGATAGG 938
Db 275 IleThrAlaGluGluAlaIleSerHisGluTrpIleSerGlyAsnAlaLaSerAspLys 294
QY 939 GACATCCTGGGTCTCTCAGTGAGCAGATCCAGAGAATTTTCCAGGACCCCACTGGAAG 998
Db 295 AsnIleLysAspGlyValCysAlaGlnIleGluLysAsnPheAlaArgAlaLysTrpLys 314
QY 999 CGTGCAATTCATGCCACATCATCTTCACGTACATCCGTAAGCTGGGACAAAAGC----- 1052
Db 315 LysAlaValArgValThrThrLeuMetLysArgLeuArgAlaProGluGlnSerGlyThr 334
QY 1053 -----CGAGGGTGAGGAGCCCTCCAGCAGTGTATGACCCGTATAGCCACCCAGGC 1106
Db 335 AlaAlaThrSerAspAlaAlaThr-ProGlyAlaAlaGlyGlyAlaValAlaAla---Al 353
QY 1107 CTTGGCAGTAGCCAGTCCCGCCAGTGTGAAAGTGTGAAACAGGTAGATGCCAAGGAAGCAAGT 1166
Db 353 alaGlyGlyAlaAlaProAlaSerGlyAlaSerAlaThrValGlyThrGlyGlyAspAl 373
QY 1167 GGACTGACTCCCGGTTTTTTCTTCCTCCAGCCCTTTTGGTCTCTTCTCGATCCTTGTGTC 1226
Db 373 agly-----CysAlaAlaLysSe 379
QY 1227 CTCACAGCTGGCTCTGCTGGAAGTCTGAGACT 1260
Db 379 rAspAspMetAlaSerAlaAspArgSerAlaThr 390

RESULT 10
T30814
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C;Species: Fugu rubripes
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C;Accession: T30814
R;Cottage, A.J.; Clark, M.; Hawker, K.; Umtania, Y.; Wheller, D.; Bishop, G.; Elgar, G.
FEBS Lett. 443, 370-374, 1999
A;Title: Three receptor genes for plasminogen related growth factors in the genome of
A;Reference number: Z20880; MUID:99148833; PMID:10025966
A;Accession: T30814
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-421 <COT>
A;Cross-references: UNIPROT:Q9YGM4; EMBL:AJ010348; NID:e1355080; PID:e1355083; PIDN:CAA
C;Genetics:
A;Introns: 32/2; 76/2; 101/2; 147/3; 186/1; 211/2; 257/1; 283/2; 312/3

Alignment Scores:
Pred. No.: 7,81e-24 Length: 421
Score: 705.00 Matches: 147
Percent Similarity: 59.12% Conservative: 67
Best Local Similarity: 40.61% Mismatches: 116
Query Match: 24.55% Indels: 32
DB: 2 Gaps: 5
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QY 495 GGCATCGTCACCGGACCTCAAGCCCTGAAACCTCTCTATGCCACACCTTTTGGAGC 554
Db 131 GlyValValHisArgAspLeuLysProGluAsnLeuLeuAlaSerLysAlaLysGly 150
QY 555 TCCAAGATCATGTCTCTGATTTGGCCTCTCC---AAATACAAGCTGGCAACATG--- 608
Db 151 AlaAlaValLysLeuAlaAspPheGlyLeuAlaIleGluValGlnGlyAspHisGlnAla 170
QY 609 ---CTAGGCACACCTGTGGGACCCAGGATATGTGCCCCAGAGCTCTCGGAGCAGAAA 665
Db 171 TrpPheGlyPheAla---GlyThrProGlyTyLeuSerProGluValLeuLysLysGlu 189
QY 666 CCCTACGGGAAGCGGTAGATGTGTGGCCCTCGGTCTCATCTCTACATCTCTGCTGTGT 725
Db 190 ProTyrglyLysSerValAspIleTrpAlaCysGlyValIleLeuTyrlleLeuLeuVal 209
QY 726 GGGTACCCCTCTTATGATGAGAGCGATCTCTGAACCTCTTCAGCCAGATTCGTAGGGCC 785
Db 210 GlyTy-ProbProPheTrpAspGluAspHisAspArgLeuTyrsSerGlnIleLysAlaGly 229
QY 786 AGCTATGAGTTGACTCCCTCTTTGGATGACATCTCAGAATCAGCCAAAGACTTCATT 845
Db 230 AlaTyAspTyrsProSerProGluTrpAspThrValThrProGluAlaLysAsnLeuIle 249
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RESULT 15
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C;Species: Drosophila melanogaster
C;Date: 30-Jun-1992 #sequence revision 14-May-1999 #text_change 09-Jul-2004
C;Accession: C44412; A44412; JU0270
R;Onoako, S.; Nishida, Y.; Ryo, H.; Yamauchi, T.
J. Biol. Chem. 268, 2052-2062, 1993
A;Title: Molecular characterization and expression of the Drosophila Ca2+/calmodulin-dep
native splicing.
A;Reference number: A44412; MUID:93131962; PMID:8380587
A;Accession: C4412
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-218; 'HD', 221-516 <OHS1>
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A;Experimental source: head
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R;Cho, K.O.; Wall, J.B.; Pugh, P.C.; Ito, M.; Mueller, S.A.; Kennedy, M.B.
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Neuron 7, 439-450, 1991
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A;Map position: 4 102E/F
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A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threon
A;Note: acts on a variety of intracellular proteins; alpha and beta chains are expresse
C;Superfamily: Ca2+/calmodulin-dependent protein kinase II; protein kinase homology
C;Keywords: alternative splicing; ATP; autophosphorylation; calmodulin binding; phospho
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F;1-346,373-516/Product: Ca2+/calmodulin-dependent protein kinase II alpha chain, 55.5K
F;12-272/Domain: protein kinase homology <KIN>
F;20-28/Region: protein kinase ATP-binding motif
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F;43,61,136,138/Active site: Lys, Glu, Asp, Lys #status predicted
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Alignment Scores:
Pred. No.: 8.38e-20 Length: 516
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QY 609 ---CTAGGCACACCTGTGGGACCCAGGATATGTGCCCCAGAGCTCTCGGAGCAGAAA 665
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.  
OM nucleic - nucleic search, using sw model  
Run on: June 5, 2005, 22:52:50 ; Search time 7779 Seconds  
(without alignments)  
7604.046 Million cell updates/sec

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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 34239544 seqs, 19032134700 residues  
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 3          | 823.2 | 53.0        | 921    | 6     | CA978376 AGENCOURT |
| 4          | 806.2 | 51.9        | 995    | 9     | AY418572 Homo sapi |
| 5          | 686.4 | 44.2        | 742    | 5     | BUS24572 AGENCOURT |
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|   | 30 | 534.8 | 34.4 | 857  | 4 | BI545446 | 603187596          |
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VERSION AY418574.1 GI:39774534  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 995)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 995)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
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JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
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| Db         | 61  | AGAAAGGGCTCTGCTCATCTTGTGGCCCTCAAGTGCATTTCCCAAGAAAGCACTTCGGG   | 120  | Homo sapiens (human)   | SOURCE   |
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| Db         | 121   | GCAGGAGGCCCTGGTGGAATGAGATCGGGTACTTCCAGAAATCAGCATCCCAACA       | 180  | Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa;  | REFERENCE  |
| QY         | 322   | TTGTGGCTCTGGAGGAGCTCCATGAGAGTCTTCTCATCTCTACTTCTGCGCATGGAGCTGG | 381  | 1 (bases 1 to 1525)  | AUTHORS  |
| Db         | 181   | TTGTGGCTCTGGAGGAGCTCCATGAGAGTCTTCTCATCTCTACTTCTGCGCATGGAGCTGG | 240  | Li, W.B., Gruber, C., Jessee, J. and Polayes, D.   | TITLE  |
| QY         | 382   | TAAACAGTGTGTAACCTGTTTGAACGATCATGAGAGGGGCTCTTACACAGAGAAAGACG   | 441  | Full-length cDNA libraries and normalization   | REMARK   |
| Db         | 241   | TAAACAGTGTGTAACCTGTTTGAACGATCATGAGAGGGGCTCTTACACAGAGAAAGACG   | 300  | Unpublished  |  |
| QY         | 442   | CCAGCCACCTGTAGGAGGCTCTTGGCGCTCTCTACCTTCATAGCTGGGCATCG         | 501  | Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 | REFERENCE  |
| Db         | 301   | CCAGCCACCTGTAGGAGGCTCTTGGCGCTCTCTACCTTCATAGCTGGGCATCG         | 360  | 2 (bases 1 to 1525)  | AUTHORS  |
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| Db         | 361   | TGCACCGGACCTCAAGCCCTGAAACCTCTCTATGCGACACCTTTTGAGGACTCCAAAGA   | 420  | Direct Submission  | JOURNAL  |
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| Db         | 421   | TCATGTCTCTGACTTTGGCTGTCTCAAAATACAAGCTGGCAACATGCTAGGCACAGCCT   | 480  | Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr   |  |
| QY         | 622   | GTGGAGCCCAAGATATGTGGCCCGCAGAGCTCTGGAGCGAAGACCTTACGGGAAGCCG    | 681  | - Web : www.genoscope.cns.fr)  |  |
| Db         | 481   | GTGGAGCCCAAGATATGTGGCCCGCAGAGCTCTGGAGCGAAGACCTTACGGGAAGCCG    | 540  | 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  |  |
| QY         | 682   | TAGATGTGTGGGCCCTGGGTGTCATCTCTACATCTCTGTGTGGGTACCCCCCTTCT      | 741  | end enriched, double-strand cDNA was digested with Not I and cloned  |  |
| Db         | 541   | TAGATGTGTGGGCCCTGGGTGTCATCTCTACATCTCTGTGTGGGTACCCCCCTTCT      | 600  | into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library   |  |
| QY         | 742   | ATGATGAGCGATCTCTGAACTCTTTCAGCGAGATTTCTGAGGGCCAGCTATGATTTGACT  | 801  | was normalized. Library was constructed by Life Technologies, a  |  |
| Db         | 601   | ATGATGAGCGATCTCTGAACTCTTTCAGCGAGATTTCTGAGGGCCAGCTATGATTTGACT  | 660  | division of Invitrogen.  | FEATURES   |
| QY         | 802   | CCCCCTTTGGGATGACATCTCAGATCAGCCAGCAAGACTTCATTCGCCACCTTCTGGAAC  | 861  | Location/Qualifiers  |  |
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| QY         | 1102  | CAGGCTTGGGACTAGCCAGTCCCCCAAGTGGTGA                            | 1136 |  | Best Local Similarity 75.6%; Pred. No. 7.9e-206;                 |
| Db         | 961   | CAGGCTTGGGACTAGCCAGTCCCCCAAGTGGTGA                            | 995  |  | Matches 1135; Conservative 0; Mismatches 282; Indels 85; Gaps 5; |
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| DEFINITION | full-length cDNA clone CS0DI079YD13 of Placenta Cot 25-normalized |   |      |  |  |
| ACCESSION  | CR611192  |   |      |  |  |
| VERSION    | CR611192.1  | GI:50491999   |      |  |  |

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Qy 1501 CC 1502  
Db 1514 CC 1515

RESULT 3  
CA978376 921 bp mRNA linear EST 06-JAN-2003  
LOCUS AGENCOURT\_11275610 NIH\_MGC\_164 Mus musculus cDNA clone  
DEFINITION

IMAGE:30144610 5', mRNA sequence.  
CA978376  
CA978376.1 GI:27511030  
EST.  
Mus musculus (house mouse)  
Mus musculus  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-rc@mail.nih.gov  
Tissue Procurement: Dr. David Rowe and Dr. Mina  
CDNA Library Preparation: Invitrogen Corp  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
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High quality sequence stop: 721.  
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Non-normalized full-length enriched library from pooled  
mouse embryonic limb, maxilla and mandible, day 10.5 and  
11.5 (size selected for the 0.5-1 kb fragments) Cloned  
directionally, priming method: Oligo-dr. cDNA enrichment:  
>1k bp, Average insert size 1.8k bp. Priming sequence:  
5'GACTAGTCTTAGATCGGAGCGGCCCTTT 3'. Tissue contributed  
by: David Rowe. Library constructed by ResGen, Invitrogen  
Corp."  
Query Match 53.0%; Score 823.2; DB 6; Length 921;  
Best Local Similarity 99.6%; Pred. No. 6.9e-204;  
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Qy 577 TTGGCTGTCCAAATACAGCTGGCAACATGCTAGGCACAGCTGTGGGACCCCGAGAT 636  
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Qy 757 CTGAACCTCTTCCAGCAGATTTCTAGGCGCAGCTATGAGTTTGATCTCCCTTTTGGGATG 816  
Db 249 CTGAACCTCTTCCAGCAGATTTCTAGGCGCAGCTATGAGTTTGATCTCCCTTTTGGGATG 307  
Qy 817 ACATCTCAGAAATCAGCCAAAGACTTCAATCGCCACCTTTCTGGAAACGTGATCCCGCAGAGA 876  
Db 308 ACATCTCAGAAATCAGCCAAAGACTTCAATCGCCACCTTTCTGGAAACGTGATCCCGCAGAGA 367  
Qy 877 GGTTCACCTCCGAGCGGCCCTTACAGCATCTTTGGATCTCTGGGGATGTCAGCCTTCGATA 936  
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| Qy  | 937  | GGGACATCTCTGGGTTCTGTGATGAGCAGATCCAGAGAAATTTTGGCAGGACCCACTGGA   | 996  |
| Db  | 428  | GGGACATCTCTGGGTTCTGTGATGAGCAGATCCAGAGAAATTTTGGCAGGACCCACTGGA   | 487  |
| Qy  | 997  | AGCGTCATTTCAATGCCACATCATTTCTACGTCACATCCGTAAGCTGGGACAAAGCCAG    | 1056 |
| Db  | 488  | AGCGTCATTTCAATGCCACATCATTTCTACGTCACATCCGTAAGCTGGGACAAAGCCAG    | 547  |
| Qy  | 1057 | AGGGTGAGGAGGCGCTCCAGCGAGTGTATGACCCGTCATAGCCACCCAGGCGCTTGGGACTA | 1116 |
| Db  | 548  | AGGGTGAGGAGGCGCTCCAGCGAGTGTATGACCCGTCATAGCCACCCAGGCGCTTGGGACTA | 607  |
| Qy  | 1117 | GCAGTCCCCCAAGTGGTGAAGAACAGAGTAGATGCAAGAGGAGCGCAAGTGGACTGATC    | 1176 |
| Db  | 608  | GCAGTCCCCCAAGTGGTGAAGAACAGAGTAGATGCAAGAGGAGCGCAAGTGGACTGATC    | 667  |
| Qy  | 1177 | CCGGTTTTTCTTCCCTCAGGCGCTTTTGGTCTCTTTCTCTGGATCCTTGCTCCAGACTG    | 1236 |
| Db  | 668  | CCGGTTTTTCTTCCCTCAGGCGCTTTTGGTCTCTTTCTCTGGATCCTTGCTCCAGACTG    | 727  |
| Qy  | 1237 | GCCTCTGCTGGAAAGTCTCAGACTGGGTGTGATGCATGCGCACTAGGCTACGGGCTTTCCC  | 1296 |
| Db  | 728  | GCCTCTGCTGGAAAGTCTCAGACTGGGTGTGATGCATGCGCACTAGGCTACGGGCTTTCCC  | 787  |
| Qy  | 1297 | CAGTATGTCGCCAGGCTCTATCTTACCTATGGTGGAGGCTCCCTTT                 | 1344 |
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| LOCUS   |      |  |      |
| DEFINITION  |      |  |      |
| Homo sapiens HCM6602 gene, VIRTUAL TRANSCRIPT, partial sequence,<br>genomic survey sequence.  |      |  |      |
| ACCESSION   |      |  |      |
| AY418572  |      |  |      |
| VERSION   |      |  |      |
| AY418572.1 GI:39774532  |      |  |      |
| KEYWORDS  |      |  |      |
| GSS.  |      |  |      |
| SOURCE  |      |  |      |
| Homo sapiens (human)  |      |  |      |
| ORGANISM  |      |  |      |
| Homo sapiens  |      |  |      |
| Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;<br>Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.   |      |  |      |
| REFERENCE   |      |  |      |
| 1 (bases 1 to 995)  |      |  |      |
| AUTHORS   |      |  |      |
| Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,<br>Todd,M.A., Tanenbaum,D.M., Civeillo,D.R., Lu,F., Murphy,B.,<br>Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,<br>Adams,M.D. and Cargill,M.<br>Infering nonneutral evolution from human-chimp-mouse orthologous<br>gene trios |      |  |      |
| TITLE   |      |  |      |
| Science 302 (5652), 1960-1963 (2003)  |      |  |      |
| JOURNAL   |      |  |      |
| PUBMED  |      |  |      |
| 14671302  |      |  |      |
| REFERENCE   |      |  |      |
| 2 (bases 1 to 995)  |      |  |      |
| AUTHORS   |      |  |      |
| Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,<br>Todd,M.A., Tanenbaum,D.M., Civeillo,D.R., Lu,F., Murphy,B.,<br>Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,<br>Adams,M.D. and Cargill,M.<br>Direct Submission  |      |  |      |
| TITLE   |      |  |      |
| Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,<br>Rockville, MD 20850, USA  |      |  |      |
| COMMENT   |      |  |      |
| These sequences were made by sequencing genomic exons and ordering<br>them based on alignment.  |      |  |      |
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| 877; Conservative   |      |  |      |
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| 118; Indels   |      |  |      |
| 0; Gaps   |      |  |      |
| 0;  |      |  |      |

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| Qy              | 142  | GTGTCATATGAGATCCGGGAGAACTGGGCTCGGTGCTCTTCTCTGAGGTGATGCTGGCCC    | 201  |
| Db              | 1    | GGGTCTACGAGATCCGGAGAGGCTCGGCTCGGTGCTCTTCTCCGAGGTGGTGTGTCGCC     | 60   |
| Qy              | 202  | AGGAAAGGGGCTCTGCTCATCTTGTGGCCCTCAAGTGCATTTCCCAAGAAAGCACTTCGGG   | 261  |
| Db              | 61   | AGGAGCGGGGCTCGCACACCTCGTGGCCCTCAAGTGCATCCCAAGAAAGGCCCTCCGGG     | 120  |
| Qy              | 262  | GCAAGAGGCCCCTGGTGGAGAAATGAGATCGCGGTACTTCGCAGAAATCAGCCATCCCCAACA | 321  |
| Db              | 121  | GCAAGAGGCCCCTGGTGGAGAAACGAGATCGCAGTCTCCGTAGGATCAGTCACCCCAACA    | 180  |
| Qy              | 322  | TTGTGGCTCTGGAGGAGTCCATGAGAGTCCCTTCTCATCTCTACTTGGCCATGAGAGTGG    | 381  |
| Db              | 181  | TCGTGCTCTGAGGAGTGTCCACGAGAGCCCTTCCACCTCTACTCTGGCCATGGAACTGG     | 240  |
| Qy              | 382  | TAAACAGGTGGTAACTGTTTTCACCGCATCATGGAGCGGGCTCCTACACAGAGAAAGACG    | 441  |
| Db              | 241  | TGACGGGTGGAGCTGTTTGACCGCATCATGGAGCGGGCTCCTACACAGAGAAAGATG       | 300  |
| Qy              | 442  | CCAGCCACTTTGTAGGCGAGTCTTGTGGCGTGTCTCTACTTTCATAGCCTTGGGCATCG     | 501  |
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| Db              | 361  | TGCACGGGACCTCAAGCCCGAAAACCTCTCTGTATGCGACGCCCTTTGAGGAGACTCGAAGA  | 420  |
| Qy              | 562  | TCATGCTCTGACTTTTGGCCTGTCCAAAATACAAGCTGGCAACATGCTAGGCAACAGCCT    | 621  |
| Db              | 421  | TCATGCTCTGACTTTTGGACTCTCCAAAATCCAGGCTGGGAACATGCTAGGCAACCGCCT    | 480  |
| Qy              | 622  | GTGGACCCCAGGATATGTGCCCCAGAGTCTCTGGAGCAGAAACCTTACGGGAAGCGCG      | 681  |
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| Qy              | 682  | TAGATGTGTGGCCCTGGGTGTCTCTCTACATCCTGTGTGGGTACCCGCCCTTCT          | 741  |
| Db              | 541  | TAGATGTGTGGCCCTTGGGCGTCACTCTCTACATCTCTGTGTGGGTACCCGCCCTTCT      | 600  |
| Qy              | 742  | ATGATGAGAGCGATCCTGAACTCTTCAGCCAGATTTCTGAGGGCCAGCTATGAGTTTGACT   | 801  |
| Db              | 601  | ACGACGAGAGCGACCTTGAGCTCTTCAGCAGATCCTGAGGCCAGCTATGAGTTTGACT      | 660  |
| Qy              | 802  | CCCCCTTTTGGATGACATCTCAGATCAGCCAAAGACTTCATTTCGGCACCTTCTGGAAC     | 861  |
| Db              | 661  | CTTCCTTTCTGGGATGACATCTCAGAAATCAGCCAAAGACTTCATCCGGCACCTTCTGGAGC  | 720  |
| Qy              | 862  | GTGATCCCCAGAAAGGTTACCTTGCCAGCAGGCCCTACAGCATCTTTTGGATCTCTGGGG    | 921  |
| Db              | 721  | GAGACCCCAGAAAGGTTCACTTGCACAAAGGCTTGGCGCACCTTTTGGATCTCTGGGG      | 780  |
| Qy              | 922  | ATGACGCTTCGATAGGGACATCTCTGGGTCTCTGTGATGAGCAGATCCAGAAAGATTTTG    | 981  |
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| Qy              | 982  | CCAGACCCACTGGAAGCGTGCATTCATGCGCATCATTTCTACGTACATCCGTAAGC        | 1041 |
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| Qy              | 1102 | CAGGCTTTGGGACTAGCAGTCCCCCAAGTGGTGA                              | 1136 |
| Db              | 961  | CAGGCTCTCGTGTGGCCAGGCCCCCAAGTGGTGA                              | 995  |
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| BUS24572        |      |   |      |
| LOCUS           |      |   |      |
| 742 bp          |      |   |      |
| mRNA            |      |   |      |
| linear          |      |   |      |
| EST 13-SEP-2002 |      |   |      |



DEFINITION AGENCOURT 10100571 NIH MGC 144 Mus musculus cDNA clone  
IMAGE:6532158 5', mRNA sequence.  
ACCESSION BU524572  
VERSION BU524572.1 GI:22835011  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Dr. Michael Brownstein  
cDNA Library Preparation: Michael Brownstein Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LICM2686 row: k column: 06  
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(ggccattatggc); Site 2: SfiI (ggccctgggc); cDNA made  
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adaptors were used in cloning as follows:  
5'-AAGCATGGTATCAACGAGTGGCCATTACGCGGG-3' and  
5'-ATTCTAGAGCCGAGGCGGCACATG-dt(30)NN-3'. Full-length  
enriched library was constructed using the Clontech  
Creator SMART kit and size-selected to contain the 0.2-0.5  
kb size fraction (other fractions present in NIH\_MGC\_143).  
Library created in the laboratory of M. Brownstein (NIH).  
NIH). Note: this is a NIH\_MGC Library."

FEATURES  
source

RESULT 6  
BF582563  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BF582563 832 bp mRNA linear EST 12-DEC-2000  
602094540F1 NCI\_CGAP\_Co24 Mus musculus cDNA clone IMAGE:420888 5',  
mRNA sequence.  
BF582563  
BF582563.1 GI:11656275  
EST.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 832)  
NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM9773 row: p column: 09  
High quality sequence stop: 717.  
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Site 2: Sall; Cloned unidirectionally. Primer: Oligo dt.  
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Technologies. Note: this is a NCI\_CGAP Library."

## ORIGIN

Query Match 44.28; Score 686.4; DB 5; Length 742;  
Best Local Similarity 99.74; Pred. No. 4e-168;  
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QY 246 AAGAAAGCACTCGGGCAAGAGGCGCCCTGGTGAGAAATGAGATCGCGGTCTTCGAGA 305  
DB 63 AAGAAAGCACTCGGGCAAGAGGCGCCCTGGTGAGAAATGAGATCGCGGTCTTCGAGA 122  
QY 306 ATCAGCCATCCCAACATTTGGCTCTGGAGGACGTTCATGAGATCTTCTCATCTCTAC 365  
DB 123 ATCAGCCATCCCAACATTTGGCTCTGGAGGACGTTCATGAGATCTTCTCATCTCTAC 182  
QY 366 TTGGCCATGGAGCTGGTAAAGAGTGGTGAAGTCTTTCACCGCATCATGGAGCGGGGTCC 425  
DB 183 TTGGCCATGGAGCTGGTAAAGAGTGGTGAAGTCTTTCACCGCATCATGGAGCGGGGTCC 242  
QY 426 TACACAGAGAGGACGCCAGCCACTTTGAGGGCAGGTCTCTTGGCGTGTCTCTACCTT 485  
DB 243 TACACAGAGAGGACGCCAGCCACTTTGAGGGCAGGTCTCTTGGCGTGTCTCTACCTT 302  
QY 486 CATAGCTTGGCATCTGTCACCGGGACCTCAAGCTGGAACCTCTCTATGCGACACCT 545  
DB 303 CATAGCTTGGCATCTGTCACCGGGACCTCAAGCTGGAACCTCTCTATGCGACACCT 362

QY 546 TTTGAGGAGCTCCCAAGATCATGTGTCTGACTTTGGGCTGTCCAAATACAAAGCTGCGAAC 605  
DB 363 TTTGAGGAGCTCCCAAGATCATGTGTCTGACTTTGGGCTGTCCAAATACAAAGCTGCGAAC 422  
QY 606 ATGCTAGGACACACCTGTGGGACCCAGGATATGTGGCCCGGAGCTCTCTGGAGCAGAAA 665  
DB 423 ATGCTAGGACACACCTGTGGGACCCAGGATATGTGGCCCGGAGCTCTCTGGAGCAGAAA 482  
QY 666 CCCTAGCGGAAGGCCCTAGATGTGTGGGCGCTGGTGTCTATCTCTACATCTCTGCTGTGT 725  
DB 483 CCCTAGCGGAAGGCCCTAGATGTGTGGGCGCTGGTGTCTATCTCTACATCTCTGCTGTGT 542  
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FEATURES  
source

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Site 2: Sall; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.6 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."

## ORIGIN

Query Match 43.9%; Score 682; DB 2; Length 832;  
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Matches 768; Conservative 0; Mismatches 30; Indels 8; Gaps 6;  
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Db 25 GCAGACATGCTGCTGCTCAAGAAACAGACGGAGGACATCAGAGTGTCTATGAGATCCGG 84  
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Db 85 GAGAACTGGCTCGGCTCGGCTGCTTCTCTGAGGTGATGCTGCCCCAGGAAAGGGCTCTGCT 144  
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Qy 338 CGTCCATGAGAGCTCTTCTCATCTCTACTTTGGCCATGAGCTGGTAACAGGTGGTGAAC 397  
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Qy 458 GCAGTCTTGGGCTGCTCTCTACCTTCTATAGCTCTGGCATGCTGCACCGGACCTCAA 517  
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Db 805 AGAAGAGTTTCACTTGCCAGAGGCC 830

RESULT 7  
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DEFINITION Pan troglodytes HCM6602 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION AY418573  
VERSION AY418573.1 GI:39774533  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pan.  
REFERENCE 1 (bases 1 to 964)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,P., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous

gene trios  
Science 302 (5652), 1960-1963 (2003)  
14671302  
2 (bases 1 to 964)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,P., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT These sequences were made by sequencing genomic exons and ordering  
them based on alignment  
FEATURES  
Location/Qualifiers  
source  
1..964  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
-1..>964  
/locus\_tag="HCM6602"  
ORIGIN  
Query Match 43.4%; Score 675; DB 9; Length 964;  
Best Local Similarity 76.6%; Pred. No. 4.1e-165;  
Matches 738; Conservative 0; Mismatches 226; Indels 0; Gaps 0;  
Qy 173 GGGTGCCTTCTCTGAGTGTATGCTGGCCAGGAAAGGGGCTCTGCTCATCTTTGTGGCCCT 232  
Db 1 GGGTGCCTNNCCGAGTGTGCTGGCCAGGAGCGGGCTCCGCACACCTCTGTGGCCCT 60  
Qy 233 CAAGTGCATTCACCAAGAAAGCACTTCGGGCAAGGAGGCCCTTGTGGAGATGAGATCGC 292  
Db 61 CAAGTGCATTCACCAAGAGGCCCTTCGGGCAAGGAGGCCCTTGTGGAGAACAGATCGC 120  
Qy 293 GGTACTTCAGAAATCAGGCATCCCAACATTTGGGCTCTGGAGAGCTCCATCAGAGTCC 352  
Db 121 AGTGCTCGTAGATCAGTCAACCCCAACATCGTCTCTGGAGATGTCCACAGAGCCC 180  
Qy 353 TTCTCATCTCTACTTTGGCCATGGAGCTGTGTAACAGGTGTGAACTGTTTGACCGCATCAT 412  
Db 181 TTCCCACTCTACTTGGCCATGGAACTGGTGACGGGNNCGAGCTGTTTGACCGCATCAT 240  
Qy 413 GGAGCGGGGCTCTACACAGAGAGACCGCCACCTTGTAGGACAGTCTTGTGGCGC 472  
Db 241 GGAGCGGGGCTCTACACAGAGAGAGATGCCACCCANNNGGTGGGTGAGTCTTGTGGCGC 300  
Qy 473 TGTCTCTACTCTATAGCTTGGGCTCGTGCAACCGGACCTCAAGCTTGAAACCTCTCT 532  
Db 301 CGTCTCTACTCTGACAGCTGGGATCGTGCAACCGGACCTCAAGCCCGGAAACCTCTCT 360  
Qy 533 CTATGCCACACCTTTTGGAGACTTCAAGATCATGGTCTCTGACTTTTGGCCTGTCCAAAT 592  
Db 361 GTATGCCACGCCCTTTGAGGACTCGAAGATCATGGTCTCTGACTTTTGGACTCTCCAAAT 420  
Qy 593 ACAGCTGGCAACATCTAGGACAGCCCTGTGGAGCCCGGAGGATGTGTGGCCCGCAGAGCT 652  
Db 421 CCAGGCTGGGAACATGCTAGGACCCCGCTGTGGAGCCCGCTGGATATGTGGCCCGCAGAGCT 480  
Qy 653 CTTGGAGCAGAAACCTCTACGGGAAGCCGTAGATGTGTGGGCGCTGGGTGTCTCTCTA 712  
Db 481 CTTGGAGCAGAAACCTCTACGGGAAGCCGTAGATGTGTGGGCGCTGGGTGTCTCTCTA 540  
Qy 713 CATCTCTGCTGTGTGGGTACCCCTTCTATGATGAGAGCGATCTCTGAACTCTTTACGCCA 772  
Db 541 CATCTNN 600  
Qy 773 GATCTGAGGGCAGCTATGAGTTGACTCCCTTTTGGGATGACATCTCAGATCAGC 832  
Db 601 NNN 660  
Qy 833 CAAAGACTTTCATTCGGCACCTTCTGGAAACGTGATCTCCCAAGAGGTTTCACTGCCAGCA 892  
Db 661 CAAAGACTTTCATTCGGCACCTTCTGGAGCGAGAGCCCGCCAGAGAGGTTTCACTGCCAACA 720

| QY                        | 993   | GGCCCTACAGCATCTTTGGATCTCTGGGGATGAGCCTTCGATAGGAGCATCTCGTGGGTTTC  | 952                    |
|---------------------------|---|---|------------------------|
| Db                        | 721   | GGCCTTCGGCGACCTTTTGGATCTCTGGGGACACAGCCTTCGACAGGAGCATCTTAGGCTC   | 780                    |
| QY                        | 953   | TGTCAGTGAGCAGATCCAGAAAGAAATTTTGCAGGAGCCACTTGGAAAGCGTGCAATCAATGC | 1012                   |
| Db                        | 781   | TGTCAGTGAGCAGATCCGGAAGAATCTTTGCTCGGACACACTTGGAAAGCAGCCTTCAATGC  | 840                    |
| QY                        | 1013  | CACATCATTTCTTACGTCCACATCCGTAAGCTGGGACAAAGCCAGAGGTTGAGGAGGCTC    | 1072                   |
| Db                        | 841   | CACCTCGTTCTTGGCCACATCCGGAAGCTGGGSCAGATCCCAGAGGCGAGGGGGCTC       | 900                    |
| QY                        | 1073  | CAGGAGTGATGACCCGTCATAGCCACCCAGGCTTGGGACTAGCAGATCCCCCAAGTG       | 1132                   |
| Db                        | 901   | TGAGCAGGGGATGGCCGCCACAGCCACTCAGGCTCCATGCTGCGCCAGCCGCCCAAGTG     | 960                    |
| QY                        | 1133  | GTGA 1136   |                        |
| Db                        | 961   | GTGA 964  |                        |
| RESULT 8                  |   |   |                        |
| CB192924                  |   |   |                        |
| LOCUS                     | CB192924  | 932 bp  | linear EST 05-FEB-2003 |
| DEFINITION                | AGENCOURT_11214785 NIH MGC_135 Mus musculus cDNA clone  |   |                        |
|                           | IMAGE:30133689 5', mRNA sequence.   |   |                        |
| ACCESSION                 | CB192924  |   |                        |
| VERSION                   | CB192924.1  | GI:28215131   |                        |
| KEYWORDS                  | EST.  |   |                        |
| SOURCE                    | Mus musculus (house mouse)  |   |                        |
| ORGANISM                  | Mus musculus  |   |                        |
| REFERENCE                 | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   |   |                        |
| AUTHORS                   | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  |   |                        |
| TITLE                     | 1 (bases 1 to 932)  |   |                        |
| JOURNAL                   | NIH-MGC <a href="http://mgs.nci.nih.gov/">http://mgs.nci.nih.gov/</a> .   |   |                        |
| COMMENT                   | National Institutes of Health, Mammalian Gene Collection (MGC)<br>Unpublished (1999)<br>Contact: Robert Strausberg, Ph.D.<br>Email: rgs@nih.gov<br>Tissue Procurement: Dr. David Rowe<br>cDNA Library Preparation: Invitrogen Corp<br>cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)<br>DNA Sequencing by: Agencourt Bioscience Corporation<br>Clone distribution: MGC clone distribution information can be<br>found through the I.M.A.G.E. Consortium/LNL at:<br><a href="http://image.llnl.gov">http://image.llnl.gov</a><br>Plate: NDAM0028 row: 0 column: 10<br>High quality sequence stop: 574.<br>Location/Qualifiers<br>1. 932<br>/organism="Mus musculus"<br>/mol_type="mRNA"<br>/db_xref="taxon:10090"<br>/clone="IMAGE:30133689"<br>/lab_host="DH10B (phage-resistant)"<br>/clone_lib="NIH_MGC_135"<br>/notes="Vector: pCMVSPORT6.1; Site 1: EcoRV; Site 2: NotI;<br>Normalized full-length enriched library from pooled mouse<br>embryonic limb, maxilla and mandible, day 12.5, 13.5,<br>14.5, and 15.5 (size selected for the 0.5-1 kb fragments)<br>Cloned directionally, priming method: Oligo-dT, cDNA<br>enrichment: 21k bp, Average insert size 1.6k bp.<br>Normalization (Cot value): 7.5 kb. Priming sequence:<br>5'-GACATGTTCTATGTCGAGGCGCCGCTT3' Tissue contributed<br>by, David Rowe. Library constructed by ResGen, Invitrogen<br>Corp." |   |                        |
| FEATURES                  | source  |   |                        |
| ORIGIN                    |   |   |                        |
| Query Match               | 42.1%   | Score 654.2; DB 6; Length 932;                                  |                        |
| Best Local Similarity     | 96.3%   | Pred. No. 1.1e-159;   |                        |
| Matches 702; Conservative | 0; Mismatches 23; Indels 4; Gaps 3;   |   |                        |

National Institute of Infectious Diseases  
23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan  
Email: khashi@nih.go.jp  
URL: http://www.nih.go.jp/yoken/genbank/.

## FEATURES

source

1..787  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL"  
/db\_xref="taxon:10090"  
/clone="MNCb-4938"  
/sex="female"  
/dev\_stage="adult"  
/lab\_host="TOP10"  
/notes="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA was primed with an oligo(dT) primer  
ATGTGGCTTTTCTTTTCTTTT; double-stranded cDNA was ligated to a DraIII adaptor [TGTGGCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3. XhoI sites just outside the DraIII sites can be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5 kb. Library was constructed by Sugano et al.(University of Tokyo, Institute of Medical Science). Custom primer used for sequencing: 5' end primer [CTTCTGCTCTAAAGCTGG], 3' end primer [CGACCTGCAGCTCGAGCACA]"

## ORIGIN

Query Match 41.6%; Score 646.2; DB 1; Length 787;  
Best Local Similarity 99.2%; Pred. No. 1.3e-157;  
Matches 659; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
QY 98 CGCAGACATGCTGCTCTCAAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCG 157  
DB 122 CCAGACATGCTGCTGCTCAAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCG 181  
QY 158 GGAGAACTGGGCTCGGGTGCCTTCTCTGAGGTGATGCTGCCAGAGAAAGGGCTCTGC 217  
DB 182 GGAGAACTGGGCTCGGGTGCCTTCTCTGAGGTGATGCTGCCAGAGAAAGGGCTCTGC 241  
QY 218 TCATCTTTGGCCCTCAAGTGCATTCACAGAAAGCACTTCGGGGCAAGGAGGCCCTGGT 277  
DB 242 TCATCTTTGGCCCTCAAGTGCATTCACAGAAAGCACTTCGGGGCAAGGAGGCCCTGGT 301  
QY 278 GGAGAAATGAGATCGCGTACTTCCAGAAATCAGCCATCCCAACATTGTGCTCTGGAGGA 337  
DB 302 GGAGAAATGAGATCGCGTACTTCCAGAAATCAGCCATCCCAACATTGTGCTCTGGAGGA 361  
QY 338 CGTCCATGAGAGTCCCTTCTCATCTCTACTTGGCCATGGAGCTGGTAAACAGGTGGTGAAT 397  
DB 362 CGTCCATGAGAGTCCCTTCTCATCTCTACTTGGCCATGGAGCTGGTAAACAGGTGGTGAAT 421  
QY 398 GTTTGACCGGATCATGAGCGGGGCTCTACACAGAAAGAGAGCCAGCCACCTTGTAGG 457  
DB 422 GTTTGACCGGATCATGAGCGGGGCTCTACACAGAAAGAGAGCCAGCCACCTTGTAGG 481  
QY 458 GCAGGTCTTTGGCGCTGTCTCTTACCTTCTAGCTGGGATCGTGACCGGAGCCCTCAA 517  
DB 482 GCAGGTCTTTGGCGCTGTCTCTTACCTTCTAGCTGGGATCGTGACCGGAGCCCTCAA 541  
QY 518 GCCTGAAAACTCTCTATGACCAACCTTTTGGAGACTTCCAAAGATCATGTCTCTGACTT 577  
DB 542 GCCTGAAAACTCTCTATGACCAACCTTTTGGAGACTTCCAAAGATCATGTCTCTGACTT 601  
QY 578 TGGCCTGTCCAAATACAGCTGCAACATGCTAGGACACAGCTGTGGACCCAGGATA 637  
DB 602 TGGCCTGTCCAAATACAGCTGCAACATGCTAGGACACAGCTGTGGACCCAGGATA 661  
QY 638 TGTGGCCCCAGAGCTCTCTGGAGCAGAAACCTTACGGGAAGGCCCTAGATGTGTGGGCC- 696  
DB 662 TGTGGCCCCAGAGCTCTCTGGAGCAGAAACCTTACGGGAAGGCCCTAGATGTGTGGGCCCT 721

QY 697 TGGGTGTCTATCTCTACATCCCTGCTGTGTGGTACCCCTTCTATGATGAGAGCGATC 756  
DB 722 TGGGTGTATCTCTCTACATCCCTGCTGTGGTGGGTACCCCTTCTATGATGAGAGCGATC 781  
QY 757 CTGA 760  
DB 782 CTGA 785  
RESULT 10  
AU080044  
LOCUS  
DEFINITION  
808 bp mRNA linear EST 12-JUL-2000  
AU080044 Sugano mouse brain mncb Mus musculus cDNA clone MNCb-5130  
5', mRNA sequence.  
ACCESSION  
AU080044  
VERSION  
AU080044.1 GI:6084799  
KEYWORDS  
EST.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelestomii;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 808)  
Hashimoto, K., Kusuda, J., Tanuma, R., Ito, A., Hirata, M., Toyoda, A.,  
Suzuki, Y., Sasaki, M. and Sugano, S.  
Isolation of full-length cDNA clones from a mouse brain cDNA  
library made by oligo-capping method  
Unpublished (1999)  
Contact: Katsuyuki Hashimoto  
Division of Genetic Resources  
National Institute of Infectious Diseases  
23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan  
Email: khashi@nih.go.jp  
URL: http://www.nih.go.jp/yoken/genbank/.  
FEATURES  
1..808  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL"  
/db\_xref="taxon:10090"  
/clone="MNCb-5130"  
/sex="female"  
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/lab\_host="TOP10"  
/clone\_lib="Sugano mouse brain mncb"  
/notes="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA was primed with an oligo(dT) primer  
ATGTGGCTTTTCTTTTCTTTT; double-stranded cDNA was ligated to a DraIII adaptor [TGTGGCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3. XhoI sites just outside the DraIII sites can be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5 kb. Library was constructed by Sugano et al.(University of Tokyo, Institute of Medical Science). Custom primer used for sequencing: 5' end primer [CTTCTGCTCTAAAGCTGG], 3' end primer [CGACCTGCAGCTCGAGCACA]"  
ORIGIN  
Query Match 40.9%; Score 636.2; DB 1; Length 808;  
Best Local Similarity 98.8%; Pred. No. 5.5e-155;  
Matches 639; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
QY 98 CGCAGACATGCTGCTCTCAAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCG 157  
DB 122 CCAGACATGCTGCTCTCAAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCG 181  
QY 158 GGAGAACTGGGCTCGGGTGCCTTCTCTGAGGTGATGCTGCCAGAGAAAGGGCTCTGC 217  
DB 182 GGAGAACTGGGCTCGGGTGCCTTCTCTGAGGTGATGCTGCCAGAGAAAGGGCTCTGC 241  
QY 218 TCATCTTTGGCCCTCAAGTGCATTCACAGAAAGCACTTCGGGGCAAGGAGGCCCTGGT 277  
DB 242 TCATCTTTGGCCCTCAAGTGCATTCACAGAAAGCACTTCGGGGCAAGGAGGCCCTGGT 301

/clone="UI-M-AQ0-cjc-i-13-0-UI"  
/dev stage="27-32 days"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NIH\_BMAP\_MHI"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not 1; Site\_2: Eco RI; The  
NIH BMAP MHI library is a non-normalized library  
constructed from mouse hippocampus. The tag is a string  
of 5 nucleotides present between the Not I site and the  
oligo-dT track. The library was constructed as described  
by Bonaldo, Lennon and Soares, Genome Research 6:  
791-806, 1996. Tissue provided by Ms. Annie Novakovich,  
Zivic-Miller Laboratories.  
TAG TISSUE=hippocampus  
TAG LIB=UI-M-AQ0  
TAG\_SEQ=TTGCGA"

ORIGIN

|                       |        |   |           |            |    |        |      |
|-----------------------|--------|---|-----------|------------|----|--------|------|
| Query Match           | 40.8%; | Score   | 633.8;    | DB         | 6; | Length | 695; |
| Best Local Similarity | 98.9%; | Pred. No.   | 2.3e-154; |            |    |        |      |
| Matches               | 690;   | Conservative  | 0;        | Mismatches | 3; | Indels | 5;   |
| Gaps                  | 5;     |   |           |            |    |        |      |
| Qy                    | 857    | GGAACTGATCCCAAGAGAGGTTTCACTGCCAGCAGGCGCTACAGCATCTTTGGATCTC    | 916       |            |    |        |      |
| Db                    | 695    | GGAACTGATCCCAAGAGAGGTTTCACTGCCAGCAGGCGCTACAGCATCTNT-GATCTC    | 638       |            |    |        |      |
| Qy                    | 917    | TGGGGATGACAGCTTCGATAGGACATCTCTGGGTTCTGTCTGAGGAGAGATCCAGAGAA   | 976       |            |    |        |      |
| Db                    | 637    | TGGGGAT-CAGCCTTCGATAGGACATCTCTGGG-TCTGTCTGAGGAGATCCAGAGAA     | 580       |            |    |        |      |
| Qy                    | 977    | TTTTGGCAGGACCCACTGGAGCGTGCAATTCATATGCCACATCATCTTCTACATCCG     | 1036      |            |    |        |      |
| Db                    | 579    | -TTTTGGCAGGACCCACTGGAGCGTGCAATTCATATGCCACATCATCTTCTACATCCG    | 521       |            |    |        |      |
| Qy                    | 1037   | TATGCTGGGACAAAGCCAGAGGTTGAGGAGGCTCCAGCAGTGATACCCGCTCATAG      | 1096      |            |    |        |      |
| Db                    | 520    | TAAAGCTGGGACAAAGCCAGAGGTTGAGGAGGCTCCAGCAGTGATACCCGCTCATAG     | 461       |            |    |        |      |
| Qy                    | 1097   | CCACCCAGGCTTTGGGACTAGCCAGTCCGCCAAGTGGTGAACACAGGTAGATGCCAAGG   | 1156      |            |    |        |      |
| Db                    | 460    | CCACCCAGGCTTTGGGACTAGCCAGTCCGCCAAGTGGTGAACACAGGTAGATGCCAAGG   | 401       |            |    |        |      |
| Qy                    | 1157   | AAGGCCAAGTGAAGTGAATCTCCCGGTTTCTTTCTCTCCAGCCCTTTTGGTCTCTTTCTG  | 1216      |            |    |        |      |
| Db                    | 400    | AAGGCCAAGTGAAGTGAATCTCCCGGTTTCTTTCTCTCCAGCCCTTTTGGTCTCTTTCTG  | 341       |            |    |        |      |
| Qy                    | 1217   | GATCTTTGCTCCAGAGCTGGCTCTGTCTGGAAAGTCTGAGACTGGGTGTGATGATGCGC   | 1276      |            |    |        |      |
| Db                    | 340    | GATCTTTGCTCCAGAGCTGGCTCTGTCTGGAAAGTCTGAGACTGGGTGTGATGATGCGC   | 281       |            |    |        |      |
| Qy                    | 1277   | ACTAGGAGTACGGGGCTTCCCGAGTATGTCCTCCAGCCCTCTATTCTTACCTATGCTGAGG | 1336      |            |    |        |      |
| Db                    | 280    | ACTAGGAGTACGGGGCTTCCCGAGTATGTCCTCCAGCCCTCTATTCTTACCTATGCTGAGG | 221       |            |    |        |      |
| Qy                    | 1337   | CTCCCTTTCCCATGTGTGCTGCCACCTCTATGAAACTGAGGAGGTGTTCAAAAGTGGAC   | 1396      |            |    |        |      |
| Db                    | 220    | CTCCCTTTCCCATGTGTGCTGCCACCTCTATGAAACTGAGGAGGTGTTCAAAAGTGGAC   | 161       |            |    |        |      |
| Qy                    | 1397   | TTGGAGCCATCTCTTCTGCACTTGTGCAAGAACATGATGATGATGATGATGATGATGATG  | 1456      |            |    |        |      |
| Db                    | 160    | TTGGAGCCATCTCTTCTGCACTTGTGCAAGAACATGATGATGATGATGATGATGATGATG  | 101       |            |    |        |      |
| Qy                    | 1457   | TTGCTGATGCTGGGTGGTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT   | 1516      |            |    |        |      |
| Db                    | 100    | TTGCTGATGCTGGGTGGTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT   | 41        |            |    |        |      |
| Qy                    | 1517   | AATAAGACAAACAGAACCAAAAAAAAAAAAAAAAAAAAAA                      | 1554      |            |    |        |      |
| Db                    | 40     | AATAAGACAAACAGAACCAAAAAAAAAAAAAAAAAAAAAA                      | 3         |            |    |        |      |

RESULT 12  
BG695422

|    |     |   |     |  |  |  |  |
|----|-----|---|-----|--|--|--|--|
| Qy | 278 | GGAGATGAGATCGCGTACTTTCGAGATCAGCATCCCAACATTTGTTGGTCTTGGAGGA    | 337 |  |  |  |  |
| Db | 302 | GGAGATGAGATCGCGTACTTTCGAGATCAGCATCCCAACATTTGTTGGTCTTGGAGGA    | 361 |  |  |  |  |
| Qy | 338 | CGTCCATGAGATCGCTTCTCATCTCTACTTGGCCATGAGCTGTAAACAGGTGTGAAT     | 397 |  |  |  |  |
| Db | 362 | CGTCCATGAGATCGCTTCTCATCTCTACTTGGCCATGAGCTGTAAACAGGTGTGAAT     | 421 |  |  |  |  |
| Qy | 398 | GTTTGACCGCATATGAGCGGGCTCTTACACAGAGAGAGAGCCAGCCACTTGTAGG       | 457 |  |  |  |  |
| Db | 422 | GTTTGACCGCATATGAGCGGGCTCTTACACAGAGAGAGAGCCAGCCACTTGTAGG       | 481 |  |  |  |  |
| Qy | 458 | GCAGGTCTTGGCGCTGTCTCTACCTTCATAGCTGGGCATCTGTGACCGGACCTCAA      | 517 |  |  |  |  |
| Db | 482 | GCAGGTCTTGGCGCTGTCTCTACCTTCATAGCTGGGCATCTGTGACCGGACCTCAA      | 541 |  |  |  |  |
| Qy | 518 | GCCTGAAACCTCTCTATGACCAACCTTTTGGAGATCTCAAGATCATGTCTGTGACTT     | 577 |  |  |  |  |
| Db | 542 | GCCTGAAACCTCTCTATGACCAACCTTTTGGAGATCTCAAGATCATGTCTGTGACTT     | 601 |  |  |  |  |
| Qy | 578 | TGGCTCTCAAATACAGCTGCAATGCTAGCAGCAGCCTGTGGGACCCAGGATA          | 637 |  |  |  |  |
| Db | 602 | TGGCTCTCAAATACAGCTGCAATGCTAGCAGCAGCCTGTGGGACCCAGGATA          | 661 |  |  |  |  |
| Qy | 638 | TGTGGCCCCAGAGCTCTCTGGAGCAGAAACCTTACGGGAAGCCGCTAGATGTGTGGGCCCT | 697 |  |  |  |  |
| Db | 662 | TGTGGCCCCAGAGCTCTCTGGAGCAGAAACCTTACGGGAAGCCGCTAGATGTGTGGGCCCT | 721 |  |  |  |  |
| Qy | 698 | GGGTGTCATCTCTACATCTCTGTGTGTGGGTACCCCTTCTAT                    | 743 |  |  |  |  |
| Db | 722 | GGGTGTCATCTCTACATCTCTGTGTGTGGGTACCCCTTCTAT                    | 767 |  |  |  |  |

RESULT 11  
CD776443/c  
LOCUS  
DEFINITION  
UI-M-AQ0-cjc-i-13-0-UI.s1 NIH BMAP MHI Mus musculus cdna clone  
EST. 02-JUL-2003  
CD776443  
UI-M-AQ0-cjc-i-13-0-UI 3', mRNA sequence.  
CD776443.1 GI:32434945  
EST.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Bonaldo, M.F., Lennon, G. and Soares, M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)  
97044477  
8889548  
Contact: Chin, H  
National Institute of Mental Health  
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
20892-9643, USA  
Tel: 301 443 1706  
Fax: 301 443 9890  
Email: m8st@mail.nih.gov  
cdna Library preparation: Dr. M. Bento Soares, University of Iowa  
cdna Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com).  
Seq primer: M13 FORWARD  
POLYA=Yes.  
Location/Qualifiers  
1..695  
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FEATURES  
source

LOCUS  
DEFINITION NISC\_iv17c03.w2 Soares NMBP2 pituitary Mus musculus cDNA clone  
IMAGE:4318060 5', mRNA sequence.  
ACCESSION BG695422  
VERSION BG695422.1 GI:13955322  
KEYWORDS EST,  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 628)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-@email.nih.gov  
cDNA Library Preparation: M. Bento Soares Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC)  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[infoimage.llnl.gov](http://infoimage.llnl.gov)  
MGI:1598828  
Plate: LLAM9923 row: E column: 5  
Seq primer: T7 primer.  
Location/Qualifiers  
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/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="Soares NMBP2 pituitary"  
/notes="Organ: brain; Vector: pT73D-Pac; Site 1: NotI;  
Site 2: EcoRI; 1st strand cDNA was primed with a NotI -  
oligo(dT) primer  
5'-AATCGGAAGATTCGCGCGCGCGCTTTTCTTTTCTTTTCTTTT-3';  
double-stranded cDNA was ligated to EcoRI adaptors  
5'-AATTCGACACAGG-3' AND 5'-CTCTGTGCGG-3' (Pharmacia),  
digested with NotI and cloned into the NotI and EcoRI  
sites of the pT73D-Pac1 vector. Library went through one  
round of normalization, and was constructed in the  
laboratory of M. Bento Soares (University of Iowa)."

FEATURES  
source

Query Match 40.4%; Score 628; DB 4; Length 628;  
Best Local Similarity 100.0%; Pred. No. 7.3e-153;  
Matches 628; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 788 CTATGAGTTTACATCCCTTTTGGGATGACATCTCAGATCAGCCAAAGACTTCATTCG 847  
DB 1 CTATGAGTTTACATCCCTTTTGGGATGACATCTCAGATCAGCCAAAGACTTCATTCG 60  
QY 848 CCACCTTTCTGGAAGCTGATCCCAAGAGAGGTTTCACTGCGCAGCAGCCCTACAGCATCT 907  
DB 61 CCACCTTTCTGGAAGCTGATCCCAAGAGAGGTTTCACTGCGCAGCAGCCCTACAGCATCT 120  
QY 908 TTGATCTCTGGGATGAGCCTTCGATAGGAGCATCTCTGGTTCCTCAGTACAGAGAT 967  
DB 121 TTGATCTCTGGGATGAGCCTTCGATAGGAGCATCTCTGGTTCCTCAGTACAGAGAT 180  
QY 968 CCAGAGATTTTCCAGGACCCACTGGAGCGGTCATTCATGCCACATCTCCTACG 1027  
DB 181 CCAGAGATTTTCCAGGACCCACTGGAGCGGTCATTCATGCCACATCTCCTACG 240  
QY 1028 TCACATCCGTAAGCTGGGACAAAGCCAGAGGGTGAGAGGCTTCCAGGAGGTGTATGAC 1087  
DB 241 TCACATCCGTAAGCTGGGACAAAGCCAGAGGGTGAGAGGCTTCCAGGAGGTGTATGAC 300

## ORIGIN

Query Match 40.4%; Score 628; DB 4; Length 628;  
Best Local Similarity 100.0%; Pred. No. 7.3e-153;  
Matches 628; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 788 CTATGAGTTTACATCCCTTTTGGGATGACATCTCAGATCAGCCAAAGACTTCATTCG 847  
DB 1 CTATGAGTTTACATCCCTTTTGGGATGACATCTCAGATCAGCCAAAGACTTCATTCG 60  
QY 848 CCACCTTTCTGGAAGCTGATCCCAAGAGAGGTTTCACTGCGCAGCAGCCCTACAGCATCT 907  
DB 61 CCACCTTTCTGGAAGCTGATCCCAAGAGAGGTTTCACTGCGCAGCAGCCCTACAGCATCT 120  
QY 908 TTGATCTCTGGGATGAGCCTTCGATAGGAGCATCTCTGGTTCCTCAGTACAGAGAT 967  
DB 121 TTGATCTCTGGGATGAGCCTTCGATAGGAGCATCTCTGGTTCCTCAGTACAGAGAT 180  
QY 968 CCAGAGATTTTCCAGGACCCACTGGAGCGGTCATTCATGCCACATCTCCTACG 1027  
DB 181 CCAGAGATTTTCCAGGACCCACTGGAGCGGTCATTCATGCCACATCTCCTACG 240  
QY 1028 TCACATCCGTAAGCTGGGACAAAGCCAGAGGGTGAGAGGCTTCCAGGAGGTGTATGAC 1087  
DB 241 TCACATCCGTAAGCTGGGACAAAGCCAGAGGGTGAGAGGCTTCCAGGAGGTGTATGAC 300

QY 1088 CCGTCATAGCCACCCAGGCGCTTGGGACTAGCCAGTCCCGCCAGTGGTGAACCAGGTAG 1147  
DB 301 CCGTCATAGCCACCCAGGCGCTTGGGACTAGCCAGTCCCGCCAGTGGTGAACCAGGTAG 360  
QY 1148 ATGCCAAGGAAGCCAAAGTGGACTGACTCCCGGTTTTTCTTTCTCCAGCCCTTTTGGTC 1207  
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QY 1208 TCTTTCTCGATCTTGTCTCCAGACTGGCTCTCTCGTGGAAAGTCTGAGACTGGGTGTG 1267  
DB 421 TCTTTCTCGATCTTGTCTCCAGACTGGCTCTCTCGTGGAAAGTCTGAGACTGGGTGTG 480  
QY 1268 ATGCATGGCACTAGGTAGCGGGCTTCCCGAGTATGTCGCCAGCCCTCTATTCTTACCTA 1327  
DB 481 ATGCATGGCACTAGGTAGCGGGCTTCCCGAGTATGTCGCCAGCCCTCTATTCTTACCTA 540  
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RESULT 13  
BG702279  
LOCUS

DEFINITION 602683496F1 NIH\_MGC\_95 Homo sapiens cDNA clone IMAGE:4816366 5',  
mRNA sequence.  
ACCESSION BG702279  
VERSION BG702279.1 GI:13973462  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-@email.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
Toshiyuki and Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM10714 row: O column: 23  
High quality sequence stop: 798.FEATURES  
source

Location/Qualifiers  
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/clone\_lib="NIH\_MGC\_95"  
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(gtcgag); Oligo-dT primed using primer  
5'-TTTCTTTTCTTTTCTTTT-3', size-selected for average  
insert size 2.5 kb and normalized to ROT 5. This is a  
primary library enriched for full-length clones and  
constructed using the Cap-trapper method (Carninci, in  
preparation). Library constructed by M. Brownstein  
(NIH/NHGRI, National Institutes of Health). Note: this  
is a NIH\_MGC Library."

## ORIGIN

|  |    |  |
|--|----|--|
| Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.      |    |  |
| 1 (bases 1 to 822)   |    |  |
| NIH-MGC http://mgc.nci.nih.gov/.                                 |    |  |
| National Institutes of Health, Mammalian Gene Collection (MGC)   |    |  |
| Unpublished (1999)   |    |  |
| Contact: Robert Strausberg, Ph.D.                                |    |  |
| Email: cgabs-i@mail.nih.gov                                      |    |  |
| Tissue Procurement: Miklos Palkovits, M.D., Ph.D.                |    |  |
| cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki |    |  |
| Toshiyuki and Piero Carninci (RIKEN)                             |    |  |
| cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)        |    |  |
| DNA Sequencing by: Incyte Genomics, Inc.                         |    |  |
| Clone Distribution: MGC clone distribution information can be    |    |  |
| found through the I.M.A.G.E. Consortium/LLNL at:                 |    |  |
| http://image.llnl.gov  |    |  |
| Plate: LLAM11653 row: m column: 05                               |    |  |
| High quality sequence stop: 778.                                 |    |  |
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| /lab_host="DH10B"  |    |  |
| /clone_lib="NIH_MGC_95"  |    |  |
| /notes="Organ: brain; Vector: pBluescriptR (modified             |    |  |
| pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI               |    |  |
| (gtcgag); Oligo-dT primed using primer                           |    |  |
| 5'-TTTTTTTTTTTTTTVN-3', size-selected for average                |    |  |
| insert size 2.5 kb and normalized to ROT 5. This is a            |    |  |
| primary library enriched for full-length clones and              |    |  |
| constructed using the Cap-trapper method (Carninci, in           |    |  |
| preparation). Library constructed by M. Brownstein               |    |  |
| (NIH/NHGRI, National Institutes of Health). Note: this           |    |  |
| is a NIH_MGC Library."   |    |  |
| ORIGIN   |    |  |
| Query Match 40.2%; Score 624.6; DB 4; Length 822;                |    |  |
| Best Local Similarity 86.5%; Pred. No. 6e-152;                   |    |  |
| Matches 712; Conservative 0; Mismatches 109; Indels 2; Gaps 2;   |    |  |
| Qy   | 48 | AGGTGG |

QY 528 CTCTCTATGCCACACCTTTTGGAGCTCAAGATCATGTCTCTGACTTTGGCCCTGTCC 587  
Db 481 CTCTCTATGCCACGCGCTTTGGAGCTCGAAGATCATGTCTCTGACTTTGGACTCTCC 540  
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Db 541 AAAATCAGGCTGGGAACATGCTAGGCACGCGCTGTGGGACCCCTGGATATGTGGCCCA 600  
QY 648 GAGCTCTCGGAGCAGAAACCTTACGGGAAGCCGTAGATGTGTGGGCCCTGGGTGTATC 707  
Db 601 GAGCTCTGGAGCAGAAACCTTACGGGAAGCCGTAGATGTGTGGGCCCTGGCGTATC 660  
QY 708 TCCTACATCTGCTGTGTGGTACCCGCCCTTCTATATGATGAGAGCATCTGAATCTTT 766  
Db 661 TCCTACATCTGCTGTGTGGTACCCGCCCTTCTACGACGAGAGCAGCTGAGCTCTT 720  
QY 767 CAGCCAGATCTGAGGGCCAGCTATGAGTTTGTAGCTCCGCCCTTTTGGGATGACATCTCAGA 826  
Db 721 CAGCCAGATCTGAGGGCCAGCTATGAGTTTGTAGCTCCGCCCTTTTGGGATGACATCTCAGA 780  
QY 827 ATCAGCCAAAGACTTCAATGCCACCTTCTGGAACGTGATCCC 869  
Db 781 ATCAGCCAAAGACTTCAATGCCCA-CTTCTGGAGCAGACCCC 822

RESULT 15  
BM986320  
LOCUS BM986320 751 bp mRNA linear EST 25-MAR-2002  
DEFINITION EST531228 Rat gene index, normalized rat, norvegicus Rattus  
norvegicus cDNA clone RGIAE45 5' end similar to  
Ca2+/calmodulin-dependent protein kinase I beta 2, mRNA sequence.  
BM986320  
ACCESSION BM986320.1 GI:19705709  
VERSION  
KEYWORDS  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus

REFERENCE 1 (bases 1 to 751)  
AUTHORS Malek R.L., Cho J., Lee Y., Karamycheva, S., Parvizi B., Perte, G.,  
Sultana, R., Tsai, J., White, J., Quackenbush, J. and Lee, N.H.  
TITLE Generation of ESTs from a rat multiple tissue survey  
JOURNAL Unpublished (2001)  
COMMENT Other ESTs: EST345697  
Contact: Lee, NH  
The Institute for Genomic Research  
9712, Medical Center Drive, Rockville, MD 20850, USA  
Tel: (301)-838-3529  
Fax: (301)-838-0208  
Email: nhlee@tigr.org  
This clone is available through the ATCC  
tel#703-365-2700 for further information  
Seq primer: M13 reverse.

FEATURES  
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/note="Vector: p7T3Pac; Site 1: EcoRI; Site 2: NotI;  
Combination of untreated and NGF-treated PC12 cell  
libraries, and Bento Soares normalized libraries of ovary,  
brain, kidney, liver, placenta, lung, embryo, skeletal  
muscle, spleen, heart"

## ORIGIN

Query Match 40.1%; Score 622.6; DB 5; Length 751;  
Best Local Similarity 94.9%; Pred. No. 2e-151;  
Matches 654; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

QY 502 TGCACCGGACCTCAAGCCTGAAACCTCTCTATGCCACACCTTTTGGAGCTTCCAAGA 561  
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QY 562 TCATGTCTCTGACTTTGGCCCTGTCCAAAATCAAGCTGGCAACATGCTAGGCACAGCCT 621  
Db 118 TCATGTCTCTGACTTTGGCCCTGTCCAAAATCAAGCTGGCAACATGCTAGGCACAGCCT 177  
QY 622 GTGGGACCCACGAGATATGTGGCCCGCAGAGCTCTGGAGCAGAAACCTTACGGGAAGCCG 681  
Db 178 GTGGGACCCACGAGATATGTGGCCCGCAGAGCTCTGGAGCAGAAACCTTACGGGAAGCCG 237  
QY 682 TAGATGTGTGGCCCTGGGTGTATCTCTACATCTCTGTGTGGTGTGGTGTGGTGTCT 741  
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QY 742 ATGATGAGAGCGATCTGAACTCTTCCAGCCAGATCTTCTGAGGGCCAGCTATGAGTTTGACT 801  
Db 298 ATGATGAGAGCGATCTGAACTCTTCCAGCCAGATCTTCTGAGGGCCAGCTATGAGTTTGACT 357  
QY 802 CCCCCTTTTGGGATGACATCTCAGAAATCAGCCAAAGACTTTCATTCGCGCACCTTCTGGAAC 861  
Db 358 CTCCCCTTTTGGGATGACATCTCAGAAATCAGCCAAAGACTTTCATTCGCGCACCTTCTGGAAC 417  
QY 862 GTGATCCCGCAGAGAGGTTTCACTGCGCAGCAGGCCCTTACAGCATCTTTGGATCTCTGGG 921  
Db 418 GTGATCCCGCAGAGAGGTTTCACTGCGCAGCAGGCCCTTACAGCATCTTTGGATCTCTGGG 477  
QY 922 ATGACGCTTTCCGATAGGAGCATCTCTGGGTCTCTCAGTGAGCAGATCCAGAGAAATTTTG 981  
Db 478 ATGACGCTTTCCGATAGGAGCATCTCTAGTTCTCTCAGTGAGCAGATCCAGAGAAATTTTG 537  
QY 982 CCAGGACCCACGAGCGTGCATTCATTCGCGCACATCTTCTACGTCACATCCGTAAGC 1041  
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QY 1042 TGGGACAAAGCCCGAGAGGTTGAGGAGCCCTCCAGGAGTGTATGACCCGCTATAGCCACC 1101  
Db 598 TGGGACAAAGCCCGAGAGGTTGAGGAGCCCTCCAGGAGGTTATGACCCGCTATAGCCACC 657  
QY 1102 CAGGCTTTGGGACTAGCCAGTCCCGCAAGTGGTGAACCCAGGT-AGATGCCAAGGAAGG 1160  
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QY 1161 CCAAGTGGACTGACTCCCGGTTTTTCTTT 1189  
Db 718 CCAAGTGGACTGACTCCCTAGCTTTTCTT 746

Search completed: June 6, 2005, 05:47:25  
Job time : 7789 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 6, 2005, 05:55:06 ; Search time 233 Seconds

(without alignments)  
6830.653 Million cell updates/sec

Title: US-10-032-254A-1

Perfect score: 2872

Sequence: 1 gttcgaggtccctccactc.....caaaaaaaaaaaaaaaaaaa 1554

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2/1/USFTO\_spool\_p/US10032254/runat\_02062005\_131019\_3593/app\_query.fasta\_1.1735  
-DB=UniProt\_03 -QMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10032254 @CGN 1 159 @runat\_02062005\_131019\_3593 -NCPU=6 -ICPU=3  
-NO\_MAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID         | Description         |
|------------|--------|-------------|--------|---------------|---------------------|
| 1          | 1801   | 62.7        | 355    | 2 Q80W07      | Q80W07 mus musculus |
| 2          | 1787   | 62.2        | 343    | 2 Q9YK9       | Q9YK9 mus musculus  |
| 3          | 1769   | 61.6        | 343    | 2 Q70150      | Q70150 rattus norv  |
| 4          | 1682.5 | 58.6        | 342    | 2 Q08767      | Q08767 rattus norv  |
| 5          | 1377.5 | 48.0        | 337    | 2 Q72H4       | Q72H4 xenopus lae   |
| 6          | 1208   | 42.1        | 241    | 2 Q6P2H8      | Q6P2H8 homo sapien  |
| 7          | 1205.5 | 42.0        | 378    | 2 Q8AVN4      | Q8AVN4 xenopus lae  |
| 8          | 1200.5 | 41.8        | 382    | 2 Q8AYR2      | Q8AYR2 xenopus lae  |
| 9          | 1192.5 | 41.5        | 395    | 2 Q6GM90      | Q6GM90 xenopus lae  |
| 10         | 1188.5 | 41.4        | 374    | 1 KCCL1_MOUSE | Q91YS8 mus musculus |
| 11         | 1188.5 | 41.4        | 374    | 1 KCCL1_RAT   | Q63450 rattus norv  |
| 12         | 1184.5 | 41.2        | 370    | 1 KCCL1_HUMAN | Q4012 homo sapien   |
| 13         | 1184.5 | 41.2        | 395    | 2 Q8AYR3      | Q8AYR3 xenopus lae  |
| 14         | 1173.5 | 40.9        | 357    | 2 Q9H31       | Q9H31 homo sapien   |
| 15         | 1173.5 | 40.9        | 385    | 2 Q8IU85      | Q8IU85 homo sapien  |
| 16         | 1171.5 | 40.8        | 385    | 2 Q8BW96      | Q8BW96 mus musculus |

|    |        |      |     |              |                     |
|----|--------|------|-----|--------------|---------------------|
| 17 | 1148.5 | 40.0 | 367 | 2 Q8BW17     | Q8BW17 mus musculus |
| 18 | 1148.5 | 40.0 | 388 | 2 Q64HW3     | Q64HW3 oncorhynch   |
| 19 | 1122.5 | 39.1 | 377 | 2 Q80W64     | Q80W64 mus musculus |
| 20 | 1105.5 | 38.5 | 299 | 2 Q8BJA6     | Q8BJA6 mus musculus |
| 21 | 1073   | 37.4 | 477 | 2 Q91VB2     | Q91VB2 mus musculus |
| 22 | 1072   | 37.3 | 476 | 2 Q7TNJ7     | Q7TNJ7 rattus norv  |
| 23 | 1065   | 37.1 | 460 | 2 Q86UH5     | Q86UH5 homo sapien  |
| 24 | 1065   | 37.1 | 481 | 2 Q9Y3J7     | Q9Y3J7 homo sapien  |
| 25 | 1063   | 37.0 | 476 | 2 Q86NX5     | Q86NX5 homo sapien  |
| 26 | 1055.5 | 36.8 | 324 | 2 Q86SC3     | Q86SC3 ciona intes  |
| 27 | 1047   | 36.5 | 426 | 2 Q6PC33     | Q6PC33 brachydanio  |
| 28 | 1043.5 | 36.3 | 433 | 2 Q6P965     | Q6P965 brachydanio  |
| 29 | 1028.5 | 35.8 | 309 | 2 Q08763     | Q08763 rattus norv  |
| 30 | 1021.5 | 35.6 | 408 | 2 Q7Q142     | Q7Q142 anopheles g  |
| 31 | 1016   | 35.4 | 377 | 2 Q7TNJ6     | Q7TNJ6 rattus norv  |
| 32 | 1015.5 | 35.4 | 405 | 2 Q9V314     | Q9V314 drosophila   |
| 33 | 1014.5 | 35.3 | 332 | 2 Q6V5R5     | Q6V5R5 caenorhabdi  |
| 34 | 1014.5 | 35.3 | 348 | 2 Q9TXJ0     | Q9TXJ0 caenorhabdi  |
| 35 | 1010.5 | 35.2 | 348 | 2 Q9UAH6     | Q9UAH6 caenorhabdi  |
| 36 | 843    | 29.4 | 284 | 2 Q8IGW6     | Q8IGW6 drosophila   |
| 37 | 839    | 29.2 | 284 | 2 Q8IMB6     | Q8IMB6 drosophila   |
| 38 | 743    | 25.9 | 436 | 2 Q7SY49     | Q7SY49 brachydanio  |
| 39 | 734    | 25.6 | 385 | 2 Q98TZ2     | Q98TZ2 xenopus lae  |
| 40 | 730    | 25.4 | 473 | 1 KCC4_HUMAN | Q16586 homo sapien  |
| 41 | 728.5  | 25.4 | 436 | 2 Q6STH4     | Q6STH4 brachydanio  |
| 42 | 727    | 25.3 | 512 | 2 Q8VD20     | Q8VD20 mus musculus |
| 43 | 726    | 25.3 | 377 | 2 Q6GLS4     | Q6GLS4 xenopus lae  |
| 44 | 725    | 25.2 | 501 | 2 Q8WTT8     | Q8WTT8 homo sapien  |
| 45 | 725    | 25.2 | 501 | 2 Q9BQC9     | Q9BQC9 homo sapien  |

#### ALIGNMENTS

RESULT 1

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ID Q80W07  
AC Q80W07  
DT 01-JUN-2003 (TEMBLrel. 24, Created)  
DT 01-JUN-2003 (TEMBLrel. 24, Last sequence update)  
DE 01-MAR-2004 (TEMBLrel. 26, Last annotation update)  
DE Pnck protein (Fragment).  
GN Name=Pnck;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McQuann P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Brain;



RT "Generation and initial analysis of more than 15,000 full-length human  
RL and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [3]

RP SEQUENCE FROM N.A.  
RC STRAIN=FVB/N; TISSUE=Colon;  
RA Strausberg R.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
RN [4]

RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
EX MEDLINE=20139438; PubMed=10673339; DOI=10.1006/geno.1999.6091;  
RA Gardner H.P., Rajan J.V., Ha S.I., Copeland N.G., Gilbert D.J.,  
RA Jenkins N.A., Marquis S.T., Chodosh L.A.;  
RA "Cloning, Characterization, and Chromosomal Localization of Pnck, a  
RT Ca2+/Calmodulin-Dependent Protein Kinase.";  
RL Genomics 63:279-288(2000).

CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

DR EMBL; AB023027; BAA87926.1; -;

DR EMBL; BC055891; AAH55891.1; -;

DR EMBL; AF181984; AAF29157.1; -;

DR HSSP; Q63450; 1A06.

DR MGP; MGI-1347357; Pnck.

DR CO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.

DR GO; GO:0016740; F:transferase activity; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR InterPro; IPR011009; Kinase like.

DR InterPro; IPR000719; Prot\_kinase.

DR InterPro; IPR002290; Ser\_thr\_kinase.

DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.

DR Pfam; PF00069; Pkinase; 1.

DR ProDom; PD000001; Prot\_kinase; 1.

DR SMART; SM00220; S\_TKc; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.

DR PROSITE; PS00011; PROTEIN KINASE\_DOM; 1.

DR PROSITE; PS00108; PROTEIN KINASE\_ST; 1.

KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

SQ SEQUENCE 343 AA; 38519 MW; 1B4A28D36E7A936E CRC64;

#### Alignment Scores:

Pred. No.: 2,57e-116 Length: 343  
Score: 1787.00 Matches: 343  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 62.22% Indels: 0  
DB: 2 Gaps: 0

US-10-032-254A-1 (1-1554) x Q90YK9 (1-343)

QY 105 ATGCTGCTCTCAAGAAACAGCAGGAGCATCAGCATGCTATGATCCGGGAGAAG 164

Db 1 MetLeuLeuLeuLysLysGlnThrGluAspLysSerValTyrGluIleArgGluLys 20

QY 165 CTGGGCTGGGTGCTCTCTGAGGTGATGCTGGCCAGGAAAGGGGCTCTGCTCATCTT 224

Db 21 LeuGlySerGlyAlaPheSerGluValMetLeuAlaGlnArgGlySerAlaHisLeu 40

QY 225 GTGGCCCTCAAGTCATCCCAAGAACACTTCGGGCAAGAGGCCCTGGTGGAGAT 284

Db 41 ValAlaLeuLysCysIleProLysLysAlaLeuArgGlyLysGluAlaLeuValGluAsn 60

QY 285 GAGATCGGGTACTTCGAGAAATCAGCCATCCCAACATTTGGCTCTGGAGAGCTCCAT 344

Db 61 GluIleAlaValLeuArgGlySerHisProAsnIleValAlaLeuGluAspValHis 80

QY 345 GAGAGTCTCTCATCTCTACTTGGCCATGAGCTGGTAAACAGGTGGTGAACCTGTTGAC 404

Db 81 GluSerProSerHisLeuTyrLeuAlaMetGluLeuValThrGlyGlyGluLeuPheAsp 100

QY 405 CGCATCATGGAGCGGGCTCTCACAGAGAAAGACGCCACCTGTATGGCAGGTC 464

Db 101 ArgIleMetGluArgGlySerTyrThrGluLysAspAlaSerHisLeuValGlyGlnVal 120

QY 465 CTTGGCGCTGCTCTTACCTTCTAGCCTGGGCATCGTGCACCGGGACCTCAAGCCTGAA 524

Db 121 LeuGlyAlaValSerTyrLeuHisSerLeuGlyIleValHisArgAspLeuLysProGlu 140

QY 525 AACCTCTCTATGCCACACCTTTTGGAGACTCCAAGATCATGGTCTCTGACTTTGGCCTG 584

Db 141 AsnLeuLeuTyrAlaThrProPheGluAspSerLysIleMetValSerAspPheGlyLeu 160

QY 585 TCCAAAATCAAGCTGGCAACATGCTAGGCACAGCCTGTGGACCCCGAGATATGTGCC 644

Db 161 SerLysIleGlnAlaGlyAsnMetLeuGlyThrAlaCysGlyThrProGlyTyrValAla 180

QY 645 CCAGAGCTCTCTGGAGCAAAACCTTCGGAAGCCGTAGATGTGTGGGCCCTGGGTGC 704

Db 181 ProGluLeuLeuGluGlnLysProTyrGlyLysAlaValAspValTyrAlaIleGlyVal 200

QY 705 ATCTCTTACATCTCTGTGTGGTATCCCTTCTATGATGAGAGCGATCTCTGAATC 764

Db 201 IleSerTyrIleLeuLeuCysGlyTyrProPheTyrAspGluSerAspProGluLeu 220

QY 765 TTCAGCCAGATTCTGAGGGCCAGCTATGAGTTTGACTCCCTTTTGGGATGACATCTCA 824

Db 221 PheSerGlnIleLeuArgAlaSerTyrGluPheAspSerProPheTyrAspIleSer 240

QY 825 GAATCAGCCAAAGACTTTCCTCCACCTTCTTGGAGCGTGATCCCAAGAGAGGTTCAAC 884

Db 241 GluSerAlaLysAspPheIleArgHisLeuLeuGluArgAspProGlnLysArgPheThr 260

QY 885 TGGCAGAGCCCTTACAGCATCTTTGGATCTCTGGGGATGAGCCTTCGATAGGAGATC 944

Db 261 CysGlnGlnAlaLeuGlnHisLeuTyrIleSerGlyAspAlaAlaPheAspArgAspIle 280

QY 945 CTGGTCTCTCAGTGAGCAGATCCAGAAGATTTTCCAGGACCCACTCGAAGCGTGCA 1004

Db 281 LeuGlySerValSerGluGlnIleGlnLysAsnPheAlaArgThrHisTrpLysArgAla 300

QY 1005 TTCAATCCACATCATCTTCTACGTCACATCCGTAAGCTGGGACAAAGCCAGAGGGTCA 1064

Db 301 PheAsnAlaThrSerPheLeuArgHisIleArgLysLeuGlyGlnSerProGluGlyGlu 320

QY 1065 GAGGCTCCAGGAGTGATGACCCGTCATAGCCACCCAGGCTTGGAGACTAGCAGTCC 1124

Db 321 GluAlaSerArgGlnCysMetThrArgHisSerHisProGlyLeuGlyThrSerGlnSer 340

QY 1125 CCCAAGTGG 1133

Db 341 ProLysTrp 343

#### RESULT 3

O70150

ID O70150 PRELIMINARY; PRT; 343 AA.

AC O70150;

DT 01-AUG-1998 (TrEMBLrel. 07, Created)

DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Ca2+/calmodulin-dependent protein kinase I beta 2.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OC NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=98070455; PubMed=9405489; DOI=10.1074/jbc.272.51.32704;

RA Naito Y., Watanabe Y., Yokokura H., Sugita R., Nishio M., Hidaka H.;

RT "Isoform-specific activation and structure diversity of calmodulin

RT kinase I.";

RL J. Biol. Chem. 272:32704-32708(1997).

CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

DR EMBL; AB004267; BAA28263.1; -;

DR HSSP; Q63450; 1A06.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO: GO:0016740; F:transferase activity; IEA.  
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro: IPR011009; Kinase like.  
DR InterPro: IPR000719; Prot kinase.  
DR InterPro: IPR002290; Ser\_Thr\_pkinase.  
DR InterPro: IPR008271; Ser\_Thr\_pkin\_AS.  
DR Pfam: PF00069; Pkinase; 1.  
DR ProDom: PD000001; Prot kinase; 1.  
DR SMART: SM00220; S\_TKc; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 343 AA; 38438 MW; 994D451D809A9D80 CRC64;

Alignment Scores:  
Pred. No.: 4,65e-115 Length: 343  
Score: 1769.00 Matches: 341  
Percent Similarity: 99.42% Conservative: 0  
Best Local Similarity: 99.42% Mismatches: 2  
Query Match: 61.59% Indels: 0  
DB: 2 Gaps: 0

US-10-032-254A-1 (1-1554) x 070150 (1-343)

QY 105 ATGCTGCTCCTCAAGAAACAGCGGAGGACATCAGCAGTCTCTATGAGATCCGGGAGAAG 164  
Db 1 MetLeuLeuLeuLysGlnThrGluAspLeuSerValTyrgluileArgGluLys 20  
QY 165 CTGGGCTGGGTGCTCTCTGAGGTGATCTGCTGGCCAGGAAGGGCTCTGTCATCTT 224  
Db 21 LeuGlySerGlyAlaPheSerGluValMetLeuAlaGlnGluArgGlySerAlaHisLeu 40  
QY 225 GTGGCCCTCAAGTGCATTCCCAAGAAAGCACTTCGGGGCAAGAGGCCCTGGTGGAGAAT 284  
Db 41 ValAlaLeuLysCysIleProLysLeuAlaLeuArgGlyLysGluAlaLeuValGluAsn 60  
QY 285 GAGATCGCGTACTTCGAGAATCAGCCATCCCAACATTTGGCTCTGGAGGACGTCCAT 344  
Db 61 GluileAlaValLeuArgArgIleSerHisPheAsnileValAlaLeuGluAspValHis 80  
QY 345 GAGAGTCTTCTACTTCTACTTGGCCATGAGGTGTAACAGGTGTGTAACCTGTTTAC 404  
Db 81 GluSerProSerHisLeuTyrgluAlaMetGluLeuValThrGlyGlyGluLeuPheAsp 100  
QY 405 CGCATCATGAGCGGGCTCTACACAGAGAAGGACGCCACCTTGTAGGCGAGTC 464  
Db 101 ArgileMetGluArgGlySerTyrgluLysAspAlaSerHisLeuValGlyGlnVal 120  
QY 465 CTGGCCGCTGCTCTTACTTCTATGCTGGCATCTGTCACCGGGACCTCAAGCCTGAA 524  
Db 121 LeuGlyAlaValSerTyrgluHisSerLeuGlyileValHisArgAspLeuLysProGlu 140  
QY 525 AACCTCTCTATGCGACACCTTTTGGAGACTCCAGATCATGCTCTGACTTGGCGTG 584  
Db 141 AsnLeuLeuTyrgluAlaThrProPheGluAspSerLysileMetValSerAspPheGlyLeu 160  
QY 585 TCCAAATACAGCTGGCAACATCTAGGACAGCCCTGTGGAGCCCGGAGATATGTGGCC 644  
Db 161 SerLysileGlnAlaGlyAsnMetLeuGlyThrAlaCysGlyThrProGlyTyrgluAla 180  
QY 645 CCAGAGTCTCTGGAGCAAAACCTTACGGGAAGCCGCTAGATGTGTGGGCCCTGGGTGC 704  
Db 181 ProGluLeuLeuGluLysProTyrglyLysAlaValaAspValTyrgluAlaLeuGlyVal 200  
QY 705 ATCTCTACATCTCTGTGTGGTACCCCTCTCTATGATGAGCGATCTCGAATC 764  
Db 201 IleSerTyrgluLeuLeuCysGlyTyrgluProPheTyrgluSerGluSerProGluLeu 220  
QY 765 TTACGACGATCTCTGAGGGCCAGCTATGAGTTTGACTTCCCTTTTGGGATGACATCTCA 824  
Db 221 PheSerGlnileLeuArgAlaSerTyrgluPheAspSerProPheTyrgluAspIleSer 240

QY 825 GAATCAGCCAAAGACTTCTTCCACCTTCTGGAACTGATCCCGAAGAGGTTCCACC 884  
Db 241 GluSerAlaLysAspPheIleArgHisLeuLeuGluArgAspProGlnLysArgPheThr 260  
QY 885 TGCCAGCAGGCCCTCAGCATCTTTGGATCTCTGGGGATGCGAGCCTTCGATATGGGACATC 944  
Db 261 CysGlnGlnAlaLeuGlnHisLeuTyrglySerGlyAspAlaAlaLeuAspArgAspIle 280  
QY 945 CTGGGTTCTGTCTCAGTGAGCAGATCCAGAAAGATTTTCCAGGAGCCCACTGGAAAGCGTGCA 1004  
Db 281 LeuGlySerValSerGluGlnileGlnLysAsnPheAlaArgThrHisTyrglyAspAla 300  
QY 1005 TTCAATGCCACATCTCTAGTCTACATCCGTAAGCTGGGACAAAGCCAGAGGTGAG 1064  
Db 301 PheAsnAlaThrSerPheLeuArgHisIleArgLysLeuGlyGlnSerProGluGlyGlu 320  
QY 1065 GAGGCTCCAGGAGGTATGATACCGCTCATAGCACCCAGGCTTCGGACTAGCCAGTCC 1124  
Db 321 GluAlaSerArgGlnGlyMetThrArgHisSerHisProGlyLeuGlyThrSerGlnSer 340  
QY 1125 CCCAAGTGG 1133  
Db 341 ProLysTrp 343

RESULT 4  
ID 008767 PRELIMINARY; PRT; 342 AA.  
AC 008767; (T-EMBLrel. 04, Created)  
DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)  
DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)  
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)  
DE Protein Kinase.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RC MEDLINE=97228532; PubMed=9074610; DOI=10.1016/S0167-4838(97)00004-6;  
RA Yokokura H., Terada O., Naito Y., Hidaka H.;  
RT "Isolation and comparison of rat cDNAs encoding Ca2+/calmodulin-  
RT dependent protein kinase I isoforms."  
RL Biochim. Biophys. Acta 1338:8-12(1997).  
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
DR EMBL; D86556; BAA19879.1; -.  
DR HSP; Q63450; 1A06.  
DR GO: GO:0005524; F:ATP binding; IEA.  
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO: GO:0016740; F:transferase activity; IEA.  
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro: IPR011009; Kinase like.  
DR InterPro: IPR000719; Prot kinase.  
DR InterPro: IPR002290; Ser\_Thr\_pkinase.  
DR InterPro: IPR008271; Ser\_Thr\_pkin\_AS.  
DR Pfam: PF00069; Pkinase; 1.  
DR ProDom: PD000001; Prot kinase; 1.  
DR SMART: SM00220; S\_TKc; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 342 AA; 38463 MW; 546C464913E78A2 CRC64;

Alignment Scores:  
Pred. No.: 5,13e-109 Length: 342  
Score: 1682.50 Matches: 334  
Percent Similarity: 86.79% Conservative: 1  
Best Local Similarity: 86.53% Mismatches: 4  
Query Match: 58.58% Indels: 47  
DB: 2 Gaps: 1

US-10-032-254A-1 (1-1554) x 008767 (1-342)

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Qy 105 ATGCTGCTGCTCAAGAAACAGACGAGGACATCAGCAGTGTCTATGAGATCCGGAGAG 164
Db 1 MetLeuLeuLeuLysGlnThrGluAspIleSerSerValTyrGluIleArgGluLys 20
Qy 165 CTGGCTCGGGTCTTCTCTGAGGTGATGCTGGCCAGGAAAGGGGCTCTGCTCATCTT 224
Db 21 LeuGlySerGlyAlaPheSerGluValMetLeuAlaGlnGluArgGlySerAlaHisLeu 40
Qy 225 GTGGCCCTCAAGTCATCCCAAGAAACACCTCGGGCAAGGAGGCCCTGGTGGAGAT 284
Db 41 ValAlaLeuLysCysIleProLysLysAlaLeuArgGlyLysGluAlaLeuValGluAsn 60
Qy 285 GAGATCGGGTACTTCGAGAGATCAGCCATCCCAACATTGGGTCTGCGAGAGCTCCAT 344
Db 61 GluIleAlaValLeuArgArgIleSerHisProAsnIleValAlaLeuGluAspValHis 80
Qy 345 GAGAGTCTTCTCATCTCTACTTGGCCATGAGCTGTGTAACAGGTGGTGAATCTTTGAC 404
Db 81 GluSerProSerHisLeuTyrLeuAlaMetGluLeuValThrGlyGlyGluLeuPheAsp 100
Qy 405 CGCATCATGAGCGGGCTCTACACAGAGAGGAGCCGACCTGTAGGCGAGTC 464
Db 101 ArgIleMetGluArgGlySerTyrThrGluLysAspAlaSerHisLeuValGlyGlnVal 120
Qy 465 CTGGCGCTGTCTCTACTTCAAGCTTTCAGGACTCCAAGATCATGCTCTGATTTGGCTG 584
Db 121 LeuGlyAlaValSerTyrLeuHisSerLeuGlyIleValHisArgAspLeuLysProGlu 140
Qy 525 AACCTCTCTATGACACACCTTTTGGAGCTCCAAGATCATGCTGTCTGATTTGGCTG 584
Db 141 AsnLeuLeuTyrAlaThrProPheGluAspSerLysIleMetValSerAspPheGlyLeu 160
Qy 585 TCCAAATACAGCTGGCAACATCTAGGACAGCTGTGGACCCAGGATATGTGCC 644
Db 161 SerLysIleGlnAlaGlyAsnMetLeuGlyThrAlaCysGlyThrProGlyTyrValAla 180
Qy 645 CCAGAGCTCTCTGGAGCAAAACCTTACGGAGGCGGTAGATGTGTGGCCCTGGGTGC 704
Db 181 ProGluLeuLeuGluGlnLysProTyrGlyLysAlaValAspValTyrAlaLeuGlyVal 200
Qy 705 ATCTCTACATCTCTGCTGTGTGGTACCCTTCTATGATGAGAGCATCTGAACTC 764
Db 201 IleSerTyrIleLeuLeuCysGlyTyrProPheTyrAspGluSerAspProGluLeu 220
Qy 765 TTCAGCCAGATCTGAGGGCCAGCTATGAGTTTGACTCCCTCTTGGGATGACATCTCA 824
Db 221 PheSerGlnIleLeuArgAlaSerTyrGluPheAspSerProPheTyrAspAspIleSer 240
Qy 825 GAATCAGCCAAAGACTTTCATTCGCCACCTCTCGGAAGTGTATCCCGAGAGGTTTACC 884
Db 241 GluSerAlaLysAspPheIleArgHisLeuLeuGluArgAspProGlnLysArgPheThr 260
Qy 885 TGCCAGCAGGCCCTACAGCATCTTTGGATCTCTGGGATGCGAGCTTCGATAGGACATC 944
Db 261 CysGlnGlnAlaLeuGlnHisLeuTyrIleSerGlyAspAlaAlaLeuAspArgAspIle 280
Qy 945 CTGGTCTCTGCTGAGTACAGATCCAGAAAGATTTTGCAGGACCCATCGAAGCGTGA 1004
Db 281 LeuGlySerValSerGluGlnIleGlnLysAsnPheAlaArgThrHisTyrLysArgAla 300
Qy 1005 TTCATGCCACATCTCTACGTCACATCCGTAGCTGGGACCAAGCCAGAGGGTGCAG 1064
Db 301 PheAsnAlaThrSerPheLeuArgHisIleArgLysLeuGlyGlnSerProGlu----- 318
Qy 1065 GAGGCCTCCAGGCAGTGTATGACCCGTATAGCCACCCAGCCCTTGGGACTAGCAGTCC 1124
Db 318 ----- 318
Qy 1125 CCCAAGTGGTGAACCAACCGTAGATGCCAAGGAAGGCCAAGTGGAGTCACTCCCGTTT 1184
Db 318 ----- 318
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Qy 1185 TCTTTCTCCAGCCCTTTGGTCTCTTTCTGGATCCTTGTCTCCAGACTGGCTCTGC 1244
Db 319 -----Ala--LeuLeuIleSerPheProAspProCysProAspTyrProLeuL 335
Qy 1245 TGGAAAGCTGAGA 1258
Db 335 euGluSerProArg 339
RESULT 5
Q7T2H4 Q7T2H4 PRELIMINARY; PRT; 337 AA.
AC Q7T2H4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE C22+/calmodulin-dependent protein kinase I-like protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Kinoshita S., Sueyoshi N., Tsuge T., Suetake I., Tajima S.,
RA Kameshita I.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AB098710; BAC78445.1; -.
DR HSP; Q63450; IAO6.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; I.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 337 AA; 38405 MW; 92C417B85E7DE6DC CRC64;
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## Alignment Scores:

|                        |          |               |     |
|------------------------|----------|---------------|-----|
| Pred. No.:             | 1.05e-87 | Length:       | 337 |
| Score:                 | 1377.50  | Matches:      | 260 |
| Percent Similarity:    | 86.76%   | Conservative: | 35  |
| Best Local Similarity: | 76.47%   | Mismatches:   | 36  |
| Query Match:           | 47.96%   | Indels:       | 9   |
| DB:                    | 2        | Gaps:         | 2   |

US-10-032-254A-1 (1-1554) x Q7T2H4 (1-337)

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Qy 114 CTCAGAAACAGACGAGGACATCAGCAGTGTCTATGAGATCCGGAGAGCTGGCTCG 173
Db 7 ValLysLysLysIleGluAspIleAsnMetValTyrAsnIleLysGluLysLeuGlyAla 26
Qy 174 GGTGCTCTCTCAGGTGATGCTGGCCAGGAGGGCTCTGCTCATCTTGTGGCCCTC 233
Db 27 GlyAlaPheSerGluValValLeuAlaGlnGluLysAsnSerGluArgLeuValAlaLeu 46
Qy 234 AAGTGCAATTCACAAAGCACTTCGGGGCAAGAGGCCCTGGTGGAGAAATGAGATCGCG 293
Db 47 LysCysIleProLysLysAlaLeuArgGlyGlyGluAlaValValGluAsnGluIleAla 66
Qy 294 GTACTTCGAGATCCACCATTCACATTTGGTCTCTGGAGGACGTCCTGAGAGTCTCT 353
Db 67 ValLeuLysLysIleThrHisGlnAsnIleValSerLeuAspIleTyrGluSerPro 86
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Qy 771 CAGATTCTGAGGCCAGCTATGAGTTGACTCCCTTTGGGATGACATCTCAGAATCA 830
Db 121 GlnileLeuArgAlaSerTyrgluPheAspSerProPheTrpAspAspIleSerGluSer 140
Qy 831 GCCAAGACTTCATTCGCCACCTCTCGAAGCTGATCCCAAGAGAGGTTCACCTGCCAG 890
Db 141 AlalysaspPheIleArgHisLeuLeuGluArgaspProGlnLysArgPheThrCysGln 160
Qy 891 CAGGCCCTACAGCATCTTTGGATCTCTGGGGATCGAGCTTCGATAGGACATCTCGGT 950
Db 161 GlnalaleuArgHisLeuTrpIleSerGlyaspThrAlaPheAspArgaspIleLeuGly 180
Qy 951 TCTGTCTAGTACAGATCCAGAAGATTTTCCAGGACCCACTCGAAGCGTGCAATTCAT 1010
Db 181 SerValSerGluGlnIleArgLysAsnPheAlaArgThrHisTrpLysArgAlaPheAsn 200
Qy 1011 GCCACATCTTCCTACGTACATCGTAGTGGGACCAAGCCAGAGGGTGAGAGGCC 1070
Db 201 AlaThrSerPheLeuArgHisIleArgLysLeuGlyGlnIleProGluGlyGluGlyAla 220
Qy 1071 TCCAGGAGTGTATGACCCGTCATAGCACCCAGCCCTGGGACTAGCCAGTCCCCCAAG 1130
Db 221 SerGluGlnGlyMetAlaArgHisSerHisSerGlyLeuArgAlaGlyGlnProProlys 240
Qy 1131 TGG 1133
Db 241 Trp 241

RESULT 7
Q8AVN4 PRELIMINARY; PRT; 378 AA.
AC Q8AVN4:
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Camki-prov protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
```

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RT initiative."
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC041721; AAH41721.1; -.
DR HGSP; O63450; LA06.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_kinase_AS.
DR Pfam; PF00069; Kinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 378 AA; 42567 MW; 066A78028EF2DAA6 CRC64;

Alignment Scores:
Pred. No.: 1.12e-75 Length: 378
Score: 1205.50 Matches: 232
Percent Similarity: 79.05% Conservative: 51
Best Local Similarity: 64.80% Mismatches: 50
Query Match: 41.97% Indels: 25
DB: 2 Gaps: 5

US-10-032-254A-1 (1-1554) x Q8AVN4 (1-378)
Qy 117 AAGAAACAGAGCGGACATCAGCAGTGTCTATGAGATCCGGGAGAGCTGGGCTCGGT 176
Db 11 LysLysArgAlaGluAspIleArgAspIleTyrgluPheArgGluValLeuGlyThrGly 30
Qy 177 GCCTTCTCTGAGTGATGCTGGCCAGGAAAGGGGCTCTGCTCATCTTGGCCCTCAAG 236
Db 31 AlaPheSerGluValValLeuAlaGluGlyLysThrGlnLysLeuValAlaIleLys 50
Qy 237 TGCAATCCCAAGAAAGCATTCCGGGCAAGAGGCCCTGGTGGAGAATGAGATCGCGTA 296
Db 51 CysIleProLysLysAlaLeuGluGlyLysThrSerIleGluAsnGluAlaVal 70
Qy 297 CTTGCGAGAATCAGCATCCCAACATTGTGGCTCTGGAGGACGTCCTCATGAGAGTCTTCT 356
Db 71 LeuArgLysIleLysHisThrAsnIleValSerLeuGluAspIleTyrgluPheArgSer 90
Qy 357 CATCTCTACTTGGCCATGGAGTGGTAAACAGGTGGTGAACCTGTTGACCGCATCATGAG 416
Db 91 HisLeuTyrgluMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGlu 110
Qy 417 CGGGGCTCTACACAGAGAGGAGCCGACCATCTGTAGGGAGGTCTTGGGCGCTGTC 476
Db 111 LysGlyPheTyrgluLysAspAlaSerGlnLeuIleLysGlnIleLeuAspAlaVal 130
Qy 477 TCCTTACCTTCATAGCTGGGCATCGTCACCGGACCTCAAGCTGGAACCTCTCTCTAT 536
Db 131 LysTyrgluHisAspMetGlyIleValHisArgAspLeuLysProGluAsnLeuTyrglu 150
Qy 537 GCCACACCTTTTGGAGCTCAAGATCATGCTCTGACTTTGGCTGTGCTCAAAATACAA 596
Db 151 TyrSerIleAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysIleGlu 170
Qy 597 ---GCTGGCAACATGCTAGGCACAGCTGTGGGACCCAGGATATGTGGCCCGCAGCTC 653
Db 171 GlySerGlySerValMetSerThrAlaCysGlyThrProGlyTyrgluValAlaProGluVal 190
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|    |      |  |      |
|----|------|--|------|
| Qy | 654  | CTGAGACGAAACCTCAGGGAAGCCCTAGATGTGTGGGCCCTGGGTGTCATCTCTCTAC   | 713  |
| Db | 191  | LeuAlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyr | 210  |
| Qy | 714  | ATCTGTGTGTGGTACCCCTTCTATGATGAGAGCGATCTCTGAACCTTCAGCCAG       | 773  |
| Db | 211  | IleLeuLeuCysGlyTyrProProPheTyrAspGluAsnAspAlaLysLeuPheGluGln | 230  |
| Qy | 774  | ATTCTGAGGCCAGCTATGAGTTTGACTCCCTCTTTGGGATGACATCTCAGAACTCAGCC  | 833  |
| Db | 231  | IleLeuLysAlaGluTyrGluPheAspSerProTyrTrpAspIleSerAspSerAla    | 250  |
| Qy | 834  | AAAGACTTCATTCGCCACCTTCTCGAAGCGTATCCCAAGAGGTTTCACTGCCAGCAG    | 893  |
| Db | 251  | LysAspPheIleGlnHisLeuMetGluLysAspProAsnLysArgIleThrCysAspGln | 270  |
| Qy | 894  | GCCCTACAGCATCTTTGGATCTCTGGGGATCGACCTTCGATAGGGACATCTCGGGTTCT  | 953  |
| Db | 271  | AlaLeuGlnHisProTrpIleAlaGlyAspThrAlaLeuAspLysAsnIleHisGluSer | 290  |
| Qy | 954  | GTCAGTGAGCAGATCCAGAAATTTGCCAGGCCCTCGAGCGTGCATTCAAATGCC       | 1013 |
| Db | 291  | ValSerGluGlnIleArgLysPheAlaLysSerArgTrpLysGlnAlaPheAsnAla    | 310  |
| Qy | 1014 | ACATCATTTCTAGTCACATCCGTAAG-----CTGGGACAAAGCCAGAGGGTGAGGAG    | 1067 |
| Db | 311  | ThrAlaValValArgHisMetCargLysLeuGlnLeuGlyThrSerGlnGluGly----- | 328  |
| Qy | 1068 | GCCTCCAGGCAGTGTATGACCCGTCATAGCCACCCAGCCCTTGGAGCTAGGCAGTCCCCC | 1127 |
| Db | 329  | -----ProGlyGlnThrThrProThrSerPro                             | 337  |
| Qy | 1128 | AAGTGGTGAACACGAGTAGATGCCAAGGAGGCCAAGTGAGCTGACTCCCGGT         | 1181 |
| Db | 338  | -----CysHisgIy-----AenLeuLeuMetProGly                        | 346  |

| SQ | SEQUENCE                                   | 382 AA;  | 42976 MW;     | B64DCE142DC1A0B2 | CRC64; | 4 |
|----|--|--|---------------|------------------|--------|---|
|    | Alignment Scores:                          |  |               |                  |        |   |
|    | Pred. No.:                                 | 2,51e-75   | Length:       | 382              |        |   |
|    | Score:                                     | 1200.50  | Matches:      | 232              |        |   |
|    | Percent Similarity:                        | 78.77%   | Conservative: | 50               |        |   |
|    | Best Local Similarity:                     | 64.80%   | Mismatches:   | 51               |        |   |
|    | Query Match:                               | 41.80%   | Indels:       | 25               |        |   |
|    | DB:  | 2  | Gaps:         | 5                |        |   |
|    | US-10-032-254A-1 (1-1554) x Q8AVR2 (1-382) |  |               |                  |        |   |
| Qy | 117  | AAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGAGAACCTGGGCTCGGT     | 176           |                  |        |   |
| Db | 11   | LysIysAArgAlaGluAspIleAArgAspIleYrGluPheAArgGluValLeuGlyThrGly | 30            |                  |        |   |
| Qy | 177  | GCCTTCTCAGGTGATGCTGGCCACGAAAGGGGCTGCTCATCTTGTGGCCTCAAG         | 236           |                  |        |   |
| Db | 31   | AlaPheSerGluValLeuAlaGluMetLysThrGlnLysLeuValAlaIleLys         | 50            |                  |        |   |
| Qy | 237  | TGCATTCCCAAGAAAGCACTTCGGGGCAAGAGGCCCTGGTGGAGAAATGAGATCCGGCTA   | 296           |                  |        |   |
| Db | 51   | CysIleProLysLysAlaLeuGluGlyLysGluThrSerIleGluAsnGluIleAlaVal   | 70            |                  |        |   |
| Qy | 297  | CTTCGCAGAAATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTCATGAGAGTCTTCT    | 356           |                  |        |   |
| Db | 71   | LeuArgLysIleLysHisThrAsnIleValSerLeuGluAspIleYrGluSerArgSer    | 90            |                  |        |   |
| Qy | 357  | CATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTGTTGACCGCATCATGGAG   | 416           |                  |        |   |
| Db | 91   | HisLeuYrLeuIleMetGlnLeuValSerGlyGluLeuPheAspArgIleValGlu       | 110           |                  |        |   |
| Qy | 417  | CGGGGCTCTTACACAGAGAAGCGCAGCCACCTTGTAGGCGAGTCTCTTGGCGCTGTC      | 476           |                  |        |   |
| Db | 111  | LysGlyPheYrThrGluLysAspAlaSerGlnLeuIleLysGlnIleuAspAlaVal      | 130           |                  |        |   |
| Qy | 477  | TCCTACCTTCTATAGCCTGGGCATCGTGCCACGGGACCTCAAGCCTGAAACCTCTCTAT    | 536           |                  |        |   |
| Db | 131  | LysYrLeuHisAspMetGlyIleValHisArgAspLeuLysProGluAsnLeuLeuYr     | 150           |                  |        |   |
| Qy | 537  | GCCACACCTTTTGGAGACTCAAAGATCATGTCTCTGACTTTGGCTGTCCAAATACAA      | 596           |                  |        |   |
| Db | 151  | TyrSerMetAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysIleGlu   | 170           |                  |        |   |
| Qy | 597  | --GCTGGCACATGCTAGGCACAGCCTGTGGGACCCGAGGATATGTGGCCCGCAGCTTC     | 653           |                  |        |   |
| Db | 171  | GlySerGlySerValMetSerThrAlaCysGlyThrProGlyYrValAlaProGluVal    | 190           |                  |        |   |
| Qy | 654  | CTGGAGCAGAAACCTACGGGAAGGCCGTAGATGTGTGGGCCCTGGGTCTCATCTCTAC     | 713           |                  |        |   |
| Db | 191  | LeuAlaGlnLysProYrSerLysAlaValAspCysTrpSerIleGlyValIleAlaYr     | 210           |                  |        |   |
| Qy | 714  | ATCTGTGTGTGGTATCCCCCTTCTATGATGAGAGCGGATCTCTGAACCTCTTCAGCCAG    | 773           |                  |        |   |
| Db | 211  | IleLeuLeuCysGlyYrProProPheYrAspGluAsnAspAlaLysLeuPheGluGln     | 230           |                  |        |   |
| Qy | 774  | ATTCTGAGGCCAGCTATGAGTTTGACTCCCTTTTCGGGATGACATCTCAGAAATCAGCC    | 833           |                  |        |   |
| Db | 231  | IleLeuLysAlaGluYrGluPheAspSerProYrTrpAspAspIleSerAspAla        | 250           |                  |        |   |
| Qy | 834  | AAAGACTTCATTCCGCCACTTCTGGAAACGTATCCCCAGAGAGGTTCACTTCGCCAGCAG   | 893           |                  |        |   |
| Db | 251  | LysAspPheIleGlnHisLeuMetGluLysAspProAsnLysArgAsnThrCysAspGln   | 270           |                  |        |   |
| Qy | 894  | GCCCTACAGCATCTTTGGATCTCTGGGAGTACGACCTTCGATAGGGAATCTCTGGGTTCT   | 953           |                  |        |   |
| Db | 271  | AlaLeuGlnHisProTrpIleAlaGlyAspThrAlaLeuAspLysAsnIleHisGluSer   | 290           |                  |        |   |
| Qy | 954  | GTCAGTGAGCATCCAGAAATTTTCGCCAGGCCACTTGAACGGCTGCATTCATTCATGCC    | 101           |                  |        |   |
| Db | 291  | ValSerGluGlnIleAArgLysAsnPheAlaLysSerArgTrpLysGlnAlaPheAsnAla  | 310           |                  |        |   |
| Qy | 1014                                       | ACATCATTTCTTACGTACATCCGTAAG-----CTGGGACAAAGCCCGAGAGGTTGAGGAG   | 106           |                  |        |   |



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Db 311 ThrAlaValIleArgHisMetArgLysLeuGlnLeuGlyThrSerGlnGluGly----- 328
Qy 1068 GCCTCCAGGCGAGTGTAGCCGTCATAGCCACCCAGGCGCTTGGGACTAGCCAGTCCCGCC 1127
Db 329 -----ProGlyGlnThrProThrSerPro 337
Qy 1128 AAGTGGTGAACACCGAGTGTAGTCCAGGAAGGCGCAAGTGGAGTCACTCCCGGT 1181
Db 338 -----CysHisGly-----AsnLeuLeuMetProGly 346

RESULT 9
Q6GM90 PRELIMINARY; PRT; 395 AA.
ID Q6GM90 AC
Q6GM90 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MGC82022 protein.
GN Name=MGC82022;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Berge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Melton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
(2)
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
(3)
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC074183; AAH74183.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001009; Kinase-like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
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DR InterPro; IPR008271; Ser_thr_kin_AS.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TyrK; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 395 AA; 43896 MW; 4C788B8F828A2CC4 CRC64;

Alignment Scores:
Pred. No.: 9,19e-75 Length: 395
Score: 1192.50 Matches: 234
Percent Similarity: 77.08% Conservative: 62
Best Local Similarity: 60.94% Mismatches: 62
Query Match: 41.52% Indels: 26
DB: 2 Gaps: 6

US-10-032-254A-1 (1-1554) x Q6GM90 (1-395)
Qy 117 AAGAAACAGAGGAGGACATCAGCAGTGTCTATGATCCGGGAGAGCTGGGCTCGGT 176
Db 14 LysLysGlnValGluAspIleLysArgMetPheGlnPheLysGluValLeuGlyThrGly 33
Qy 177 GCCTTCTCTGAGGTGATGCTGGCCAGCAAGGGGCTCTGTCTATCTTGTGGCCCTCAAG 236
Db 34 AlaPheSerGluValValLeuAlaGluGluLysGluThrGlyLysLeuPheAlaValLys 53
Qy 237 TGCATTCCTCCAGAAAGCACTTCGGGGCAAGAGGAGCGCTGGTGGAGAAATAGATCCGGTA 296
Db 54 CysileProLysLysAlaLeuLysGlyLysGluSerSerileGluAsnGluAlaVal 73
Qy 297 CTTCGCGAGATCAGCCATCCCAATCTGGCTCTGAGGACGCTCCATGAGAGTCTCTCT 356
Db 74 LeuArgLysileLysHisGluAsnIleValAlaLeuGluAspIleTyrGluSerProSer 93
Qy 357 CATCTCTACTTGGCCATGGAGCTGGTAAACAGGTGGTGAACCTGTTTGACCGCATCATGAG 416
Db 94 HisLeuTyrLeuValMetGlnLeuValSerGlyGlyLeuPheAspArgIleValGlu 113
Qy 417 CGGGGCTCTCTACAGAGAGGAGCGCCAGCCACCTCTGTAGGCGAGGCTCTTGGGCGTCTC 476
Db 114 LysGlyPheTyrThrGluLysAspAlaSerThrLeuileArgGlnValLeuAspAlaVal 133
Qy 477 TCCTACCTTCATAGCTGGGCGATCGTCACCGGGACCTCAAGCTGAAAACCTCTCTAT 536
Db 134 SerTyrLeuHisArgLeuGlyIleValHisArgAspLeuLysProGluAsnLeuTyr 153
Qy 537 GCCACACCTTTTGAGGACTCCAAGATCATGTCTCTGACTTTGGGCTGTCCAAATACAA 596
Db 154 PheSerGlnValGluGluSerLysileMetileSerAspPheGlyLeuSerLysMetGlu 173
Qy 597 GCT---GGCAACATGTAGGACAGCGCTGTGGGACCCAGGATATGTGGCCCGCAGAGCTC 653
Db 174 GlyLysGlyAspValMetSerThrAlaCysGlyThrProGlyTyrValAlaProGluVal 193
Qy 654 CTGAGCAGAGAAACCTTACCGGGAAGGCGGTAGATGTGTGGGCGCTGGGTGTCATCTCTAC 713
Db 194 LeuAlaGlnLysProTyrSerLysAlaValAspCysTrpSerileGlyValIleAlaTyr 213
Qy 714 ATCTCTGTGTGGGTACCCCTTCTATGATGAGAGCGCATCTGAACCTCTTCAGGCAG 773
Db 214 IleLeuLeuCysGlyTyrProProPheTyrAspGluAsnAspSerArgLeuPheGluGln 233
Qy 774 ATTCTGAGGCGGAGCTATGATGTTTGAATCTCCCTTTTGGGATGACATCTCAGAAATCAGCC 833
Db 234 IleLeuLysAlaAspTyrGluPheAspSerProTyrTrpAspIleSerGluSerAla 253
Qy 834 AAGACTTCATTCGCCACCTCTTGGAACGTGATCCCGAGAGAGGTTTCACTGCCACGAG 893
Db 254 LysAspPheIleGlnAsnLeuMetGluLysAspProAsnLysArgTyrThrCysGluGln 273
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QY 894 GCCTACAGCATCTTGGATCTCTGGGATGTCAGCCTTCGATAGGACATCCCTGGGTCT 953
Db |||||:| |||||:| |||||:| |||||:| |||||:| |||||:| |||||:| |||||:|
274 AlaLeuArgHisProTrpIleAlaGlyAspThrAlaLeuCysAsnIleHisGluSer 293
QY 954 GTCACTGAGCAGATCCAGAGATTTTGGCAGGACCCACTGGAAGCGTGCATTCAATGCC 1013
Db |||||:| |||||:| |||||:| |||||:| |||||:| |||||:| |||||:| |||||:|
294 ValSerAlaGlnIleArgLysAsnPheAlaLysSerLysTrpArgGlnAlaPheAsnAla 313
QY 1014 ACATATTCCTACGTCACATCCGTAAG-----CTGGGACAAAAGCCAGAGGTGGAG 1067
Db |||||:| |||||:| |||||:| |||||:| |||||:| |||||:| |||||:| |||||:|
314 ThrAlaValAlaArgHisMetArgLysLeuHisLeuGlySerSerGlnAspSerSerAsn 333
QY 1068 GCCTCCAGGAGTGTATGACCCGTCATAGCCACCCAGGCGCTTGGAGTACCCAGTCCC-- 1125
Db |||||:| |||||:| |||||:| |||||:| |||||:| |||||:| |||||:| |||||:|
334 ValSer-GlyGlyAsnSerPro-----AlaSerProLe 344
QY 1126 -CCAAGTGGTCAAAACACAGGTAGATGCCAAGGAGGCCAAGTGCATGCTCCCGGTTT 1184
Db |||||:| |||||:| |||||:| |||||:| |||||:| |||||:| |||||:| |||||:|
344 uProAspGlyThrSerArgLysAspCysLysPro----- 355
QY 1185 TCCTTCCAGCCCTTTTGGTCTCTTCTCTGGA-----TCCTTGTCCTCCAGACTGCC 1238
Db |||||:| |||||:| |||||:| |||||:| |||||:| |||||:| |||||:| |||||:|
356 ----ProSerThrProTyrSerPheLeuSerGlyValSerSerAlaSerSerAlaIleSe 374
QY 1239 CTCTGTGGA 1248
Db |||||:| |||||:| |||||:| |||||:| |||||:| |||||:| |||||:| |||||:|
374 rAlaValGly 377

RESULT 10
KCC1_MOUSE
ID KCC1_MOUSE STANDARD; PRT; 374 AA.
AC Q91Y88;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type I (EC 2.7.1.123) (Cam
DE kinase I).
DE NCBI_TaxID=10090;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Baha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Beak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
PL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: Phosphorylates synapsin I (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -!- ENZYME REGULATION: Activated by Ca(2+)/calmodulin. Must be
CC phosphorylated to be maximally active.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. CamK
CC subfamily.
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FT STRAND 147 149
FT TURN 154 155
FT STRAND 158 160
FT TURN 183 184
FT HELIX 187 190
FT TURN 191 192
FT TURN 197 197
FT TURN 198 213
FT HELIX 223 231
FT TURN 232 233
FT TURN 239 244
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Alignment Scores:
Pred. No.: 1.72e-74 Length: 374
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Percent Similarity: 85.53% Conservative: 51
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Query Match: 41.38% Indels: 3
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US-10-032-254a-1 (1-1554) x KCCL_RAT (1-374)

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QY 180 TTCTCTGAGTGATGCTGGCCAGGAAAGGGCTCTCTCATCTTGTGGCCCTCAAGTGC 239
DB 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50
QY 240 ATTCACCAAGAAACACATCTCGGGGCAAGAGGCGCTGTGGAGATGAGATCGGGTACTT 299
DB 51 IleAlaLysLysAlaLeuGluGlyLysGluGlySerMetGluAsnGluIleAlaValLeu 70
QY 300 CGCAGATACGCCATCCCAATGTGCTCTGGAGACGTCCTCATGAGATCCTTCTTCAT 359
DB 71 HisLysIleLysHisProAsnIleValAlaLeuAspAspIleTyrGluSerGlyGlyHis 90
QY 360 CTCTACTTGGCCATGGAGCTGGTAACAGTGTGTGAAGTGTGACCGCATCATGGAGCGG 419
DB 91 LeuTyrLeuIleMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGluLys 110
QY 420 GGTCTCTACACAGAGAGGAGCGCCAGCACCTCTGTAGGCGAGGTCCTTGGCTGTCTCC 479
DB 111 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130
QY 480 TACCTTCATAGCTGGGCATGTGTCACCGGACCTCAAGCTCAAGCTCAAGCTCTCTATGCC 539
DB 131 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuLeuTyrTyr 150
QY 540 ACACCTTTTGGAGCTCAAGATCATGCTCTGACCTTGGCTGTGCTCAAAATACAA--- 596
DB 151 SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp 170
QY 597 GCTGGCAACATGCTAGGACAGCTGTGGGACCCAGCATATGCGCCCGAGAGCTCCTG 656
DB 171 ProGlySerValLeuSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeu 190
QY 657 GAGCAAAACCTTACGGGAAGCGGTGATGTGTGGGCCCTTGGGTGTCATCTCTCATATC 716
DB 191 AlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyrIle 210
QY 717 CTGCTGTGTGGTACCCCTCTCTATGATGAGAGCATCTCTGAACCTCTTCAGCCAGCAT 776

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Db 211 LeuLeuCysGlyTyrProProPheTyrAspGluAsnAspAlaLysLeuPheGluGlnIle 230
QY 777 CTGAGGGCCAGGTATGAGTTTGAATCTCCCTTTTGGATGACATCTCAGAAATCAGCCAAA 836
Db 231 LeuLysAlaGluTyrGluPheAspSerProTyrTrpAspAspIleSerAspSerAlaLys 250
QY 837 GACTTCATTCCGACCTCTCTGGACGTGATCCCCAGAGAGGTTCACTCCAGCAGGCC 896
Db 251 AspPheIleArgHisLeuMetGluLysAspProGluLysArgPheThrCysGluGlnAla 270
QY 897 CTACAGCATCTTTGGGATCTCTGGGATGCGAGCTCTCGATAGGAGACATCTCGGTCTGTGC 956
Db 271 LeuGlnHisProTyrTrpIleAlaGlyAspThrAlaLeuAspLysAsnIleHisGlnSerVal 290
QY 957 AGTGACGACATCCAGAAGAAATTTTGCAGAGCCCACTGGAGAGCGTGCATTCAATGCCACA 1016
Db 291 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 310
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DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type I (EC 2.7.1.123) (Cam
DE kinase I).
GN Name=CAMKI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-49.
RX MEDLINE=95369239; PubMed=7641687;
RA Haribabu B., Hook S.S., Selbert M.A., Goldstein E.G., Tomhave E.D.,
RA Edelman A.M., Snyderman R., Means A.R.;
RT "Human calcium-calmodulin dependent protein kinase I: cDNA cloning,
RT domain structure and activation by phosphorylation at threonine-177 by
RT calcium-calmodulin dependent protein kinase I kinase.";
RL EMBO J. 14:3679-3686(1995).
RN [2]
RP SEQUENCE OF 1-9.
RC TISSUE=Platelet;
RX MEDLINE=22608239; PubMed=12665801; DOI=10.1038/nbt810;
RA Gevaert K., Goethals M., Martens L., Van Damme J., Staes A.,
RA Thomas G.R., Vandekerckhove J.;
RT "Exploring proteomes and analyzing protein processing by mass
RT spectrometric identification of sorted N-terminal peptides.";
RL Nat. Biotechnol. 21:566-569(2003).
CC -1- FUNCTION: Phosphorylates synapsin I.
CC -1- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -1- ENZYME REGULATION: Activated by Ca(2+)/calmodulin. Must be
CC phosphorylated to be maximally active.
CC -1- SUBUNIT: Monomer.
CC -1- TISSUE SPECIFICITY: Ubiquitous.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. CamK
CC subfamily.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L41816; AAA99458.1; -.
CC PIR; S57347; S57347.

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DR HSP: Q63450; 1A06.  
DR Genew; HGNC:1459; CAMK1.  
DR MIW; 604998; -.  
DR GO; GO:0004685; P:calcium/calmodulin-dependent protein kinase. . .; TAS.  
DR GO; GO:0006458; P:protein amino acid phosphorylation; TAS.  
DR GO; GO:0007165; P:signal transduction; TAS.  
DR InterPro; IPR011009; Kinase-like.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR Pfam; PF00069; Pkinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00220; S\_TK; 1.  
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
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KW Phosphorylation; Serine/threonine-protein kinase; Transferase.  
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FT NP\_BIND 34 49  
FT BINDING 49 49  
FT ACT\_SITE 141 141  
FT MOD\_RES 177 177  
FT MUTAGEN 49 49 K->A: Loss of activity.  
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Pred. No.: 3 27e-74 Length: 370  
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Best Local Similarity: 69.18% Mismatches: 43  
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QY 180 TTCTCTGAGGTGATGCTGGCCAGAGAAAGGGCTCTGCTCATCTGTGGCCCTCAAGTGC 239  
DB 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50  
  
QY 240 ATTCCCAAGAACACTTCGGGGCAGAGGCCCTGTGGAGATGAGATCCGGTACTT 299  
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QY 300 CGCAGAATCAGCCATCCCAACATTTGGCTCTGGAGGACGTCATGAGAGCTTCTCAT 359  
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QY 360 CTCTACTTGGCAGTGGAGCTGTAAACAGGTGGTGAACCTGTTGACCGCATCATGGAGCG 419  
DB 91 LeuThrLeuIleMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGluLys 110  
  
QY 420 GGCTCTACAGAGAGGACGCGCCACCTTGTAGGCGAGGTCTTTGGCGCTGTCTCC 479  
DB 111 GlyPheThrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130  
  
QY 480 TACCTTCATAGCTGGGATCGTCACCGGACCTCAAGCTGAAACCTCTCTATGCC 539  
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QY 597 GCTGGCAACATGCTAGGCACAGCTGTGGGACCCCGAGGATATGGCCCGCAGAGCTCTG 656  
DB 171 ProGlySerValLeuSerThrAlaCysGlyThrProGlyThrValAlaProGluValLeu 190

QY 657 GAGCAGAAACCTCAGCGGAAAGCCGTAGATGTGTGGCCCTGGGTGTCATCTCTACATC 716  
DB 191 AlaGlnLysProThrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyrIle 210  
  
QY 717 CTGCTGTGGTACCCGCCCTTCTATGATGAGAGCGATCCTGAACCTCTTCAGCCAGATT 776  
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QY 777 CTGAGGCCAGCTATGAGTTTGATCTCCCTTTTGGGATGACATCTCAGATCAGCCAAA 836  
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QY 837 GACTTATTCGCCACCTTCTGGAAAGTATCCCGAAGAGGTTCACCTGCCAGCAGGCC 896  
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DB 291 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 310  
  
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DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Calcium/calmodulin-dependent protein kinase (CaM-KI protein).  
GN Name=CaM-KI;  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sanevoshi T., Kume S., Mikoshiba K.;  
RT "Calcium/calmodulin-dependent protein kinase I in Xenopus laevis.";  
RL Comp. Biochem. Physiol. B, Comp. Biochem. 134:499-507(2003).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Oocytes;  
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshitsuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [3]  
RP SEQUENCE FROM N.A.



DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
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DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
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DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00220; S\_TKc; 1.  
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DR PROSITE; PS00108; PROTEIN KINASE\_ST; 1.  
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 357 AA; 40189 MW; 1FA184EEPA976FB4 CRC64;  
  
Alignment Scores:  
Pred. No.: 1.9e-73 Length: 357  
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DB 177 AlaPheSerGluValValLeuAlaGluGluLysAlaThrGlyLysLeuPheAlaValLys 52  
  
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DB 357 HisLeuTyrLeuValMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGlu 112  
  
QY 417 CGGGCTCTTACACAGAGAGGACGACCCACCTGTGTAGGCGAGTCTTGGCGCTGTC 476  
DB 417 LysGlyPheTyrThrGluLysAspAlaSerThrLeuIleArgGlnValLeuAspAlaVal 132  
  
QY 477 TCCTACCTTATAGCTGGGATCGTCGACCGGACCTCAGCTGAAACCTCTCTAT 536  
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QY 537 GCCACACCTTTTGGAGCTCAAGATCATGTCTCTGACTTGGCTGTGCTCAAAATACAA 596  
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DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Calcium/calmodulin-dependent protein kinase ID, beta isoform (CaM-kinase I delta).  
GN Name=CAMK1D; Synonyms=Cam-KI delta;  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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RC TISSUE=Pancreas;  
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RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Pancreas;  
RX MEDLINE=22816754; PubMed=12935886; DOI=10.1016/S0014-5793(03)00817-2;  
RA Iehikawa Y., Tokumitsu H., Inuzuka H., Murata-Hori M., Hosoya H.,  
RA Kobayashi R.;  
RT "Identification and characterization of novel components of a  
Ca2+/calmodulin-dependent protein kinase cascade in HeLa cells.";  
RL FEBS Lett. 550:57-63 (2003).  
RN [4]

